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(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE NARROW			
(57) Abstract			
This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.			

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HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

5 Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may 10 contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

15 20 25 30 There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon genomic DNA sequencing.

35 Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., *Science* 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs 5 identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new 10 clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are 15 exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. *Gene Expression*, Vol. 2: *Eukaryotic Chromosomes*, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

20 Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

25 Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be 30 selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

35 A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to 40 large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 5 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each 10 reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 15 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered 20 to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

25 (a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;

30 (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;

35 (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and

40 (d) carrying out an extension synthesis in the mixture produced in step (c).

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

5

Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually, therefore, all DNA species will be present at the same concentration.

20 The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

25 In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first 30 primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

35 In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid 40 population is treated by:

(a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adaptored cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c) selecting and separating only those adaptored cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok 1.

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin reaction in selecting and separating desired adaptored molecules. Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adaptored molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adaptored end of 5 the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand 10 making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during 15 subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide 20 also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot 25 interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it 30 is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from 35 the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adaptoring" process can be used to generate categories or 40 subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

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- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- 15 (c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% 20 homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to 25 said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, 30 for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 35 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

40 The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that 5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or sequence in accordance with the invention may be released by the 10 endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

25 Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved 30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and 40 Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other 10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

15 It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate 20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate 25 indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence 30 fragments) could only be identified through some known characteristic [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having 35 ability to encode expressed proteins which could later be detected by functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present 40 invention are entirely underivable and unpredictable from the prior art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alessio, J. M., et al., Focus (Gibco B.R.L) 9 p1 (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targeting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eukaryotic hosts may be selected as the host for expression and higher

eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. Gene 40 p183 1985),
5 Shimuzu, Y et al., Gene 65, p141 (1988), Straus, D. and Gilbert, W. Proc. Natl. Acad. Sci. 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

10 The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith,
15 D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. Nature 353 pp605-607 (1991), Rudensky, A., Y., et al., Nature 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable, although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide.
20 25 30 35 40 Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., C. Methods Enzmol. 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising *in situ*, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg 5 cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in 10 combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease 15 states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given 20 individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 25 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, 30 Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

35 Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA 40 will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

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All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 10 (1985)).

Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age foetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, 20 using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed 25 for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA⁺ (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to 30 magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA 35 were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and 40 then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5 The column eluate was adjusted to 10 mM Mg²⁺ and then the purified cDNA was restricted by the action of 1 unit per 10 μ l of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10 The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

15 The adaptors used were oligonucleotides 5' N₄N₄N₄TCCTTCTCCTGCGACAGACAA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTCGCAGGAGAAGGA (SEQ ID: 1195) and 5' AAN₄N₄TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN₄N₄TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 20 5' biotinylated strand GTTCTCGGAGCAGTGCTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added MgCl₂ to 10mM, ATP to 10mM and 0.025 units/ μ l of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCAGTGCTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume 25 was 90 μ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

30 Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

35 The column eluate was adjusted to 25mM Mg²⁺, 0.5mM dNTPs in a final volume of 200 μ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 μ l of 40 streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

.GTTCTCGGAGCAGTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg²⁺. The beads were then resuspended in 240 µl of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60
10 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adaptored fragments. 2 pmoles of the primer 5' CTGTCTGTGCAGGAGAAGGAA
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq
DNA polymerase were added to each reaction and 16 cycles of alternate
20 denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of
25 resuspended beads were added to each reaction to remove the biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one
35 of the primers 5' GTTCTCGGAGCAGTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCAGTGTCCGAGAC SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8 μ l or 12.5 % whichever was the larger 5 but not exceeding 12 μ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg²⁺, 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40 μ l. Apart from when an initial amplification with 2 pmoles of each 10 primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. 15 Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

20 The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60 μ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris 25 HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. 30 (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75 μ l or 75 % of the column eluate, whichever was least, were added 9.5 μ l of 100mM TrisHCl pH7.4, 100 mM MgCl₂, and 9.5 μ l of 0.5 mM dTTP. 35 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as 40 described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adapting the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG 5 (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adapting were performed according to standard 10 procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 15 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. 20 CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol 25 was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing 30 templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive. 35 In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the 40 plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40 μ l reactions containing 2.5mM Mg²⁺, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of AmpliTaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of 10 successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic work-station attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. 20 Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluorescein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for 25 the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" 30 (TED). In both cases, files of called bases were entered into a SybaseTM database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the 35 publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the 40 above procedure.

Example 2

.. A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTCGACAAAGCTTGAATTCGCGGCCGC(T)₂₆, (SEQ ID: 1210) was used at 1 μ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100 μ l with water.

PCRs were then performed in reactions containing 1 μ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin, 200 μ M dNTPs, 10 uCi a³²P dCTP, 1 μ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

40 Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5

cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of 10 recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyocarcroma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15

Clear plaques from each library were resuspended in 5 μ l of Tris-HCl pH 8, 1 mM EDTA. 2 μ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that 20 the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30

Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35 The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

(1) GENERAL INFORMATION

(i) APPLICANT

5 (A) NAME: MEDICAL RESEARCH COUNCIL
(B) STREET: 20 PARK CRESCENT
(C) CITY: LONDON
(E) COUNTRY: ENGLAND
(F) POSTAL CODE: W1N 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

15 (iv) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: DISKETTE
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: EXTRACT

20 (2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCTGT GACCAAGAAG GCTCTGTGCA TTGGGGTTTT CCAGGAGACT 50

35 CAAAAGCTGA AGAACGGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA 100

ATAAAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC 150

40 CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT 200

GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCTAT ATATCATATA 250

TATATATATA CACA

264

(2) INFORMATION FOR SEQ ID :2:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15 AGGAACATGT GTTTATTCA CCAGCAGTGT TGCTCAGCTC CTACCTCTGT 50
GCCAGGGCAG CATTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC 100
CTGGGGAGGG GGTCAATTGTT CTCT 124

20

(2) INFORMATION FOR SEQ ID :3:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAACG 50
TAAGATTTCGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC 100
TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC 150
AAATTAAGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA 200
40 GCACAATCAC TACTGTAGAG ATAACAGAAT TTCTGAATT CCTGAAAGCA 250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG 300

TCACATATTA GGAACGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50

20 GGAGCTCAAG GATCAGAGTA ACACAATTT CACTTTTCT GTCTTTATGT 100

AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAAA CAGGAATTTC 150

TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCCCT CTGCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50

40 AGATTTGCCA AATTGTAGCC TACTGGATTG CGGTTCTCTT GACATCTCTT 100

TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAAA GGGAGGATT AAGAATAATG AAAAGAGAAA AATCAAGAAA	200
GCACAATCAC TAG	213

5 (2) INFORMATION FOR SEQ ID :6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG	50
GAAGTTTAA GCTAAGATT GCCAAATTGT AGCCTACTGG ATTCCGGTTC	100
20 TCTTGACATC TCTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC	150
GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG	200
25 AAAAATCAAG AAAGCACAAT CACTAGTGT AAGATAACAG AATTCTGAA	250
TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT	300
30 GTGGCCCATA CGTCACATAT TAGGAAGTGA TAACATAAGG TAAAC	345

(2) INFORMATION FOR SEQ ID :7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

	TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCCTG	50
	GGGTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCA	100
5	GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT	150
	TTCTTTCC	159

(2) INFORMATION FOR SEQ ID :8:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 124 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20	ATATTTCAAT CGAACAAAAA GGAAACTTTT TTTGAACCTTA TTGAGGCTCT	50
	ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCCT	100
25	TGCCTGGCTG GGGGTTGAT TCGC	124

(2) INFORMATION FOR SEQ ID :9:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 259 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35	(xi) SEQUENCE DESCRIPTION: SEQ ID :9:	
	CCGATACAAA TGTACGGAAT CTGTGAGTCC CTCTGGGAGC CCAACATGGA	50

40	TCCGGATCAC CTGTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG	100
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26

	ACCGGGATGC AGTGTCAAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG	150
	GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCCCTGTTC	200
5	CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA	250
	GAAAATAGA	259

(2) INFORMATION FOR SEQ ID :10:

10

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

	GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCCAGGG CCCTCAAGAA	50
	GCTCCTGCAC ACAATAAACG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT	100
25	CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA	150
	GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA	200
	CTGTGACAAG GGGCCC	216

30

(2) INFORMATION FOR SEQ ID :11:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :11:

	CACACTTCTT AAGATAACATC AAGTACTAGT GATCTTGCT AGCAGTTATG	50
	CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA	100
5	AAGTTGAAAG AAAAAGTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT	150
	GCAGGCTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG	200
	GGATG	205

10 (2) INFORMATION FOR SEQ ID :12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :12:

	TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC	50
25	AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT	100
	CACCGTCCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA	150
	GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG	200
30	TAAGTCCATG CTGCGTCAA TATTCCACTA TATTCCACAC TACTGCTGGA	250
	TATGCCATTC TCGGTGA	267

35 (2) INFORMATION FOR SEQ ID :13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTGCCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50
5 GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100
 CAATGTGAAG CTGAAC 116

10 (2) INFORMATION FOR SEQ ID :14:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

50 TTCGAACCTTA CCAGCATCAT GTTTGGTCTC TTCGTATGGT CAAACTTCAA
50 CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150
 ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATAACATCTA 200
30 AGGGGTGCAA GGACCAGGCT TTGATTCAA ATTATAATCT AATGCTCACT 250
 CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

(2) INFORMATION FOR SEQ ID :15:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :15:

CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG 50
5 AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACCTCA ACTCTTCCTC 100
CAAACACTCGAT TCAAAGAGCA ATA 123

(2) INFORMATION FOR SEQ ID :16:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20 CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT 50
GGCATTGTCA GAAAAATTAA ACAGGTTTAT TTATAATTAT CATAAAGTTG 100
25 ACGCTGAAAC TTGTTCACTG AAACATTAA ACTTGCATTA ATGCTTTACG 150
TCTCCGCATT TATATTAAAA ATTACACACAC AAATGAAATG GAAAAACTGC 200
CAATACCTGA TTTCTGTCCC TATTTTCAC TCGCAATCAT ATACTTAGTA 250
30 CTTTTGACTC TA 262

(2) INFORMATION FOR SEQ ID :17:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

10 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50
5 AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT 100
TGAAAGTAAG TTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATTT 150
TCAAGAAACG TGCAATCAGC 169

10

(2) INFORMATION FOR SEQ ID :18:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :18:

25 AGGGGCACCA TTACCATCCA TCTGACATCG CATTCCATA GAAATGGCCA 50
AAGAAAGAAG GTCCTGGTAG GTTTTCATA GAAAGACTCA AAAAGTTCAA 100
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150
TTATTAAAAT ACTGGCTTCG GTTTCTTTT TTCCTTGCA AAGTTTCCTA 200
30 CATATATGTC TTTTACAGTA T 221

30

(2) INFORMATION FOR SEQ ID :19:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

31

(xi) SEQUENCE DESCRIPTION: SEQ ID :19:

10 TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTACAA 50
5 TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTT ATGTGTTGCT 100
TCTATTTAC CTGAAATTGT AGATATAGGG TAATC 135

(2) INFORMATION FOR SEQ ID :20:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20 GTTATCTATC TATCTTGCAG TTTACCTATC TGATCTGATC TCTGTAATT 50
TAGTTCTGTC ATTAAAATA TACTATTTAA ATCTAATTAA TACATTCAA 100
25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150
TTATTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200
TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTAA AAAAAATTGT 250
30 ATAATTTGT GATAATGTAG TTTCCAAAA CACATTTAGA AAGCATTATG 300
TTATTAGTAA ATGA 314

(2) INFORMATION FOR SEQ ID :21:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCACTACA GATACTCTT CTGTACTTGC TTAATCTGCT 50
TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100
TCTGAAGATC TGCTTCAGA TTCTGGTAC GAGCAGAGCT TACAGAGAGT 150
10 TCCTCTTCA ATATTTCTGT TTCTTGCC 178

(2) INFORMATION FOR SEQ ID :22:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
20

 (xi) SEQUENCE DESCRIPTION: SEQ ID :22:
25 ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50
ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA 100
GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTT 150
30 TTTCTTAAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

(2) INFORMATION FOR SEQ ID :23:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
40

33

(xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTATA TTTTNAAAT 50
5 GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTAAATT CTCCAATT 100
TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTATCA ATTGAATTGA 150
10 GG 152

(2) INFORMATION FOR SEQ ID :24:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :24:
ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTCA ACCAACTTCA 50

25 ACTTTTGCAC ACTTTTCAA CGGTCCCACC ACA 83

(2) INFORMATION FOR SEQ ID :25:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :25:
AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA 50

40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC 150

CTACATCTGG CTGACATTAA CATTAA 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACCGCTTT TAAAATATTAA GAACAGAAAA 50

GCTACAAATA AATNGAGCAA TGCTTTAAA ATCATCTTG TTTTATAGAC 100

20 TTTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150

TTAAGTACTG ACCAAGAAGA CTAAAACAAT CATTAACTAA CAATATTAA 200

25 AAGGATCATA TAGTCGACTT TTAAAACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACCTCTCT AAGGAGAATG 50

40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AACACATTGTT TGCCTAAATA 100

35

CGCAATGCAA AATTTNNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTCG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

20 TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTAACCC CTCATAAAAT 100

GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTCAC TTTATTGGCC 50

40 CCTCCCTACA TTGGGTTAG GTTCCATTG ATTTGCACAA TAATGACTTT 100

	ATTTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTA TCATAGAACT	150
	AACTATTTA ATTACATATA ATGTAACATAA TGGAGAGATT TATAGAGAAT	200
5	TTTGTAAAAA TGTCATATAC TCCATTCGA AGACAGATAT GATAGAACTA	250
	GAAATTAAGT TGCATTTCTG CAACT	275

(2) INFORMATION FOR SEQ ID :30:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20	GTAAATNTAC AAAGATAACG TCGCAATTAA CTTAGATTTA AATCAAAGAC	50
	ATTCAATCAAC AAGATTCGA ATGGAATATT CCAGAAATTCTGAGCCATC	100
25	TGATCACAAC AACCGTCTTT GA	122

(2) INFORMATION FOR SEQ ID :31:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :31:

40	GGATTTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT	50
	AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAAATG	100

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC

150

TCGATCGCAC TAGTGCACAA CAAACACGA TGAGTGCAAT GTGAAAC

197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG

50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC

97

20

(2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA

50

35

CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATT AATAGCTCCT

100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC

150

40

AACATACAAT ACATCATTAA AATAACATAA ACGACTTTCA CACACTTGAC

200

CTAGGAAAAA ATAAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT

250

CACAATAAGA

260

(2) INFORMATION FOR SEQ ID :34:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15	GGACNTGCGC NNNANNNA N GCCANTGAAC NCAGCCACCA NTGCAAGAAG	50
	ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT	100
	GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNNGAT AAGGTGTGGA	150
20	NTTNGGTTAA AGACAAGG	168

(2) INFORMATION FOR SEQ ID :35:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35	CTCGNACACT GTGGAGAGCC TGCNNNNNN NNGGTNTACT CAGGGGGACG	50
	AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT	100
	GCTNNNGTGG TCCCTTAGNA SCCGAGNAGG TGGGCGCGAG GTGAANAAGG	150
40	TGCNNNGTGCAG AGAGTGCCTG ATT	173

(2) INFORMATION FOR SEQ ID :36:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA	50
15 CAACTAATAA TGATTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA	100
20 GTTTGCTAA CCTTGGTAAG CTTGTTTACC GTTT	134

(2) INFORMATION FOR SEQ ID :37:

20

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :37:

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA	50
35 ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTTGCTC AGTACAGACN	100
40 GATTTACAAT GAAAGTTTG CTAACCTTGG TAAGCTTGT AACCCTTAC	150
ATGACTTCTT	160

(2) INFORMATION FOR SEQ ID :38:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

10	CTAGTTAAT GAATCTGAGG GGCTACTATA AACAAATCCCA CCCTCACACG	50
	ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT	100
	CCACCTCTAT TCTCCGCACTG TCCAAGAGGC CCACCTAATC	140

15 (2) INFORMATION FOR SEQ ID :39:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 203 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :39:

	AGCAAGTATC ANNNNNNNNN ATACATTGATTCAGTTG TTTTTGTCA	50
30	AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG	100
	GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATT GCCACCACCG	150
	CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGGA	200
35	AAA	203

(2) INFORMATION FOR SEQ ID :40:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 170 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

	GAAAAGCNNN NNNNNNNNGC TTAAAGAAC A	ATATGCTGAG ATGGAGAAGG	50
	ACCTAGCGAA ANTNNNAACC TTTAAGAAC TTGAANNACA ACAATCACAA		100
10	ACTAATGAGA AGATGTTCAC CTCTCTCCTG AAAACTATGC CCACCAGACC		150
	GTTCAGCCTC TGCTCAAGCT		170

15 (2) INFORMATION FOR SEQ ID :41:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 270 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

	GCTGCATGTT TCCTGNATT TGAGCTTGAA AGTCAGAGC TGTTTACCCA	50
	AAAAGGGAGC CAATAGAGAT CTTCCAATG AACCTCAAAC ACGTCGTAAT	100
30	ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA	150
	CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA	200
35	ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTT AAATNCATAG	250
	AAATTTGATT TGTAAATAAA	270

40 (2) INFORMATION FOR SEQ ID :42:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 245 base pairs	

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :42:

	AGAGCTGCAT GTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC	50
10	CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT	100
	AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC	150
15	ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT	200
	GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTC TCTTA	245

(2) INFORMATION FOR SEQ ID :43:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 124 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30	TACACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC	50
	TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA	100
35	ATGAAGACAC TTTACACTTT TCGG	124

(2) INFORMATION FOR SEQ ID :44:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 144 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

	GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG	50
	GCAAATTCTT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTAA	100
10	AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA	144

(2) INFORMATION FOR SEQ ID :45:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25	ACTGATTCTNN NNTGAAAATA CCCCCCTTCT CCATTAGTGG CATGCTCATT	50
	CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTAA	100
	CAAAAAAAA AACAAACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA	150
30	GAAATTAAAT GTTTTCATA ACATGAA	177

(2) INFORMATION FOR SEQ ID :46:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

	ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT	50
5	TTATCTTAT ATTCAAATAA CTTATTCGC TTTCACTGTT TTAACAAAAA	100
	AAAAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTT	150
	TAATTCACAC GGAAAAACCA AGACAATTTC ACAACTTCTG GACACAACCA	200
10	TCAACACAGG ACATTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT	250
	CCCAGA	256

15 (2) INFORMATION FOR SEQ ID :47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

	GAGAAAAGTC NNNNNNNNNNA GGTTAATCTA ACTTTCTTG CTTATTCAG	50
	CTATGATCTG AAAGGATGGA AGACACAAAAA TGTATGNNTA AGGTATTTT	100
30	AACAAAGATA CATGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG	150
	AGCAA	155

35 (2) INFORMATION FOR SEQ ID :48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5	GCTTATTTA CTATATCTAA AGGATAAAGC ACAAAATGAT GAATAAGATA	50
	TTTNNACAAA GATACACG	68

(2) INFORMATION FOR SEQ ID :49:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 244 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

	(xi) SEQUENCE DESCRIPTION: SEQ ID :49:	
20	CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG	50
	GGCCTAGCTA AATTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA	100
	ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC	150
25	TCTGTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG	200
	AAGTTCCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCC ATGG	244

30 (2) INFORMATION FOR SEQ ID :50:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 81 base pairs
	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

	ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA	50
--	--	----

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15 GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA 50
AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT 100
TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT 150
20 TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTT 200
TTATACCAGA AGNATGACCA CTG 223

25 (2) INFORMATION FOR SEQ ID :52:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTNT TGTAAAAAAG CTCANNANA AAGGGANNGG CTTAAGAGA

49

40 (2) INFORMATION FOR SEQ ID :53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :53:

10	CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
	TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
	TTCTAGAGTC TATACTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
15	TCAATCTGAC TAACAAGAGN AATTGATTCA TTTCTTCCA CNCCCCTTCA	200
	TTCAATAATC AAA	213

(2) INFORMATION FOR SEQ ID :54:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 166 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

30	(xi) SEQUENCE DESCRIPTION: SEQ ID :54:	
	GC GTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG	50
	CGTNNTTGC G TANGGGGNNGG GTTTNGGCAG GTGTTGCCGG TAGCNAACN	100
35	GTGCCCCCA TNGCCNGNAT TGNNNCCCN CNNGGAANG GGGGGGGNGA	150
	CCNNAGNNGG AAAAAA	166

(2) INFORMATION FOR SEQ ID :55:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 75 base pairs	

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50
10 NGNCGTTGTN GCTGCCAAGC GACAT 75

(2) INFORMATION FOR SEQ ID :56:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25 AATNNNNNCC TATTTGTAA TTTTTTGAA AAAAGTTCAA TGTCAGTTT 50
30 TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATT CTGTGAAGCA 100
AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA 150
35 TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

(2) INFORMATION FOR SEQ ID :57:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTCAGG ATGTTGATC ACAATACGAA 50
5 GATGACGNNA TCCAATTCA GAACACCACA GGGCACTGGC ACACAGAGGG 100
GATTATTACA GAACCACTGA GATGACATTT 130

(2) INFORMATION FOR SEQ ID :58:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20 GTNATTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50
CATTGACAAG TACAAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA 100
25 GAACACAAGC CACTGTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTT 150
CCATGAA 157

(2) INFORMATION FOR SEQ ID :59:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40 GAGGTGAAGT TGTTCTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100
GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATT 150
5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200
AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250
CA 252

10

(2) INFORMATION FOR SEQ ID :60:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50
GCCTTAACCTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100
25 AAAGGAAGCA ACAAAATAATG TCGCTTTCA CCTGACGTCT GGTTCAACTT 150
TCCGCCAGC CTATTCCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

	GAGGTGGCAT TATGTGAGAC AGCATTGGT TAGGGAGTGC CAAGCATTCT	50
	ACAGCATTG ATGGTGGAAA TAGTCATGCT TTTTATTCT GCTCTCTAGG	100
5	AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAAGGTC	150
	CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGCA	200
	GAGTGCTTCT CATAACACCTT CAGGAACCC	229
10		

(2) INFORMATION FOR SEQ ID :62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :62:	
	CATCCTGGC CCTGGCCGAT GTGCATATCA ACANAAAAAA GGGACTGAAG	50
25	AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA	100
	ACCGCTTAAT GAATTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGC	150
	AAGAGCTTTT GGACTGTTT TAGAACAGAA T	181

30 (2) INFORMATION FOR SEQ ID :63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :63:	

52

	GTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA	50
	ATTTGGCAGA AACAAAGAAAA GGACATGGGA TAACTTTAG ATTTAAAGAG	100
5	GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA	150
	TAAGGCTACT CCACAAAGACC ATTAGAAGTC	180

(2) INFORMATION FOR SEQ ID :64:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID :64:	
20	ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC	50
	AGGGAACTGT GATTATTTAA AAATANGCNA GAACTTATT CANCTGTGCT	100
25	TTAGAAANAA NTGTATACGG	120

(2) INFORMATION FOR SEQ ID :65:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35	(xi) SEQUENCE DESCRIPTION: SEQ ID :65:	
40	CACATCGCTA TAATCCTTTC TGAGGACTTA AAACTTATN CCACTTACCT	50
	TTATGACTTT TAACAAAGCCT	70

(2) INFORMATION FOR SEQ ID :66:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :66:

TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT	50
15 ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG	100
GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAC	150
20 CTGGGGGACC CTTTNAAAA AACCTCCTT CAAGAGACCC TAATACTCTN	200
TCCACACACC CACACGATTT AGGAACTTGG ACATGTTCC	240

(2) INFORMATION FOR SEQ ID :67:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35 GGAAGCACTA CATTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT	50
TACGATATGC TTAGGTAGGC TTTTAACCTG CTCCTCCAAA CAATATCTNT	100
40 TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT	150
AACCTATTTG TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG	200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250

TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAGT GAAAGACTAA CCAAGATTTG 50

20 ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100

TCAACAAATN NNNACAACTG AGAACCTGGG AATTCCCGCA CGGAAGACAA 150

GAGATAACCT CTCCAATTAA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAA CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50

40 AGGAGGGCGAA TTGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC 100

CCGGGGGAAG CC 112

(2) INFORMATION FOR SEQ ID :70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT	50
TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG	100
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT	150
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG	200
CAGATTATT CCTTTAACTG ACATTTCCAT GA	232

(2) INFORMATION FOR SEQ ID :71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :71:

CNTGGATCCG NCCTTGTAC GNCCAGGACG NCTGGACCGC AAAATGAATT	50
TTCACTTTG GACCACCGCC AGAAGAGATG ATTTCTCAT CATNAACAAG	100
GAACCTTGAG GAGATCGAC TGAAAGACTA GCGNCCNGT CAGATAAGAT	150
TTAGGGCTGA	160

(2) INFORMATION FOR SEQ ID :72:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT CGTTGCCAT CCGAGATCAT TAAAANGNC TGACCCTAAC	50
15 AATACTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT	100
CTTAAAGTAC TTTAAGAAA AAAAGCAGGN CCTTGGAAAGT TTGATTCTT	150
20 TTTCCCTCCC GTCGCAAATT CTATGTTGG AT	182

20

(2) INFORMATION FOR SEQ ID :73:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG	50
35 ATGAGCTGGA CGAGCACAGC ACTAAAAGG CTTGCCCTNG CACAATAACA	100
CTGAGAGGAT GATGAGAAC A CTTGAAAT GCTTCATNCA CATGGGCAGG	150
ANAGGCTGCA CAATGAAA	168

40

(2) INFORMATION FOR SEQ ID :74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTATT CATCCTCCTN TCCAAGACCT ATGAGAACGT TCCAGGCC	50
AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCCGGGTT	100
GTATACCACA CCCCCGGGCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA	150
ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC	200
NCTNTCCCTN NAATAAATTN C	221

20

(2) INFORMATION FOR SEQ ID :75:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNNTG GGTCAATCCGA GATCATTAAA AATGNCTGAC CCTAACATA	50
GGCACAAAAAA TAAAAACGAA ATAAAAAACCC TCCTTANNTT CGAAGTATCT	100
TAGAAAAAAA CAGGGCCTTG AGTTCTG	127

40

(2) INFORMATION FOR SEQ ID :76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :76:

	AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACA TTTCAAAACC	50
10	CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAAATGACC	100
	ACAAAATTAA TACTACCAAA TCATTACTGA GACTCTTGCA TTACAATATT	150
15	TGGAGAGTAG GTGAAGAAAA TNTAGACCGA	180

(2) INFORMATION FOR SEQ ID :77:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 142 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :77:

	GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTC	50
30	GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAAACTG	100
	TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC	142

35 (2) INFORMATION FOR SEQ ID :78:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 124 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5 GGCCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNNTAGAA CCNNCAGGNT 100
CTGNCCCCCC CNNNGNCCCC CCCG 124

10 (2) INFORMATION FOR SEQ ID :79:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTCA 50
TATAGTCTAA AAGCTAGAAG AACAAAGAGTG TATTCGTGG GTGGATGTAT 100
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150
TTAAGNAAAN GCCNTTTAA G 171

30 (2) INFORMATION FOR SEQ ID :80:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 98 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACAGTGCC GTGNGGGCAT CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15 CCTCAAACAAG TGCGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG 50

CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT 100

CAACATCA 108

20

(2) INFORMATION FOR SEQ ID :82:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC 50

35 CCTAAATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA 100

GAATGTCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACAAACAACA 150

ACGCCTACGA AATTCTAAAT TCAGAAGGAA 180

40

(2) INFORMATION FOR SEQ ID :83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10	GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT	50
	CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC	100
15	GTTGGACGCA TGTTTAGATG CCTTGAGAC CGCCCAGAGA AGTCCTTGTC	150
	CTTCTTAATA AACACCTCCT CGCCAATGCG GACGACCACA ATCACCGTA	199

(2) INFORMATION FOR SEQ ID :84:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 214 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30	CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA	50
	CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA	100
35	GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG	150
	CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCCTGGCC CCTCCCATT	200
	NACNGAATAC AACC	214

(2) INFORMATION FOR SEQ ID :85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10 CCTGGGCAAG CTGAATGTGA AGTTGACCAAG GCTAACTGAG AAGCAAGCCC 50
AGTACCTGGG CATGTCCTGT GATGGCCCCT 80

15 (2) INFORMATION FOR SEQ ID :86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAACAG ACCCACATCT CTATTCTTGC 50
CCTGAAATAC GCGCTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT 100
30 CCACACGGCA TTGACGGAC ACAGAAATGT GACTGTTACC GGATAACACT 150
GATTAGTCAG TTTCATTTA TAAAAAAGCA TGACAGTTA TTACTCTGTT 200
35 TCTTTTAATG 210

(2) INFORMATION FOR SEQ ID :87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

	CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT	50
	ATTTAAAAAT ACTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA	100
10	CA	102

(2) INFORMATION FOR SEQ ID :88:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 275 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25	GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT	50
	ACGGGCAGTG AGAACATTAT CTGTATAACA GGAACTGTGA TTATTTAAAA	100
	ATAGCAGAAC TTATCNGTCT GTGCTTCTAGA AATAACTGTA TACAGTGTAA	150
30	TAAGTTGAAA AGAACTCAAA ATAACATAAA CAAATAAGAA CCTACGTATT	200
	AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAACAAA	250
35	TGACACAAAT TCAAAACACG ATCAT	275

(2) INFORMATION FOR SEQ ID :89:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

	GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA	50
	TTAATAGTAA TTATGGTTTG GNNGTAAAAT CGAGTTTCAG AATAAAATNA	100
10	AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAAGCT TTTGTTTGT	150
	TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAAGTTA AGAGTTTCC	200
15	TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT	250
	GCTGTGTACT CCA	263

(2) INFORMATION FOR SEQ ID :90:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 108 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :90:

30	GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC	50
	CACCAACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCG CGAGGGACCC	100
35	CTTTGAGA	108

(2) INFORMATION FOR SEQ ID :91:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 206 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :91:

20	GCCTTGGTGG AGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
10	ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
	TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTCAG AGCACCCACAG	150
	GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT	200
15	TAATAA	206

(2) INFORMATION FOR SEQ ID :92:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

30	CCTTGGTGG A GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
	TGGCTTTGGC TGATAGATT GAAGAGACCT CAATTACGTT TTTCAGGAAT	100
	GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTCAGA GCACCCACAGG	150
35	GCACGTGTGA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
	AATAAANNNG	210

40

(2) INFORMATION FOR SEQ ID :93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAAACT AACCTAAAAG	50
10 GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA	100
AACATGGCGA AAGGAGCTCT CTCTTCCCC GCAGTCTACC AAGCTCCTGT	150
15 GCATTTCAC CACATAGATC TGCTAGCTTA CAAATGATG	189

(2) INFORMATION FOR SEQ ID :94:

20 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 160 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG	50
30 CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC	100
TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN	150
35 GTCATTTAAT	160

(2) INFORMATION FOR SEQ ID :95:

40 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 171 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCAC TT CATAAAATTT GCATTTGGT	50
AAAAGGCAAC AATTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTT	100
10 AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTT	150
TAAGGAAACT ACAGAAGGGA T	171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT	50
TTCCCCAACC TTTTATTGCG CGAAGAACT CCAGTTGTTA ACTTTTGAG	100
30 AGTTTTTTT GGCAAAAGAA CTNCATTAN C	131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :97:

	GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA	50
5	GTAAAGTTAA GGCACGTACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA	100
	CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN	150
10	TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC	200
	ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT	250
	TTTGAATAAA TTTATNGAAC TTATGAAGA	279

(2) INFORMATION FOR SEQ ID :98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

	GTGAGTCTTT CTTCAACTAG GGGATGTTT CCAGGGCACCG CCAGGCCTCA	50
	CTCACGCAGG CCTCCGCGAC AACTGTTCACTGACTGAA GGATGAAGTG	100
30	AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA	150
	CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT	200
35	GACGAGACCA GGACCCTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA	250
	AACTCCAGGG CCTCCA	266

40 (2) INFORMATION FOR SEQ ID :99:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

10	GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA	50
	ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTGGT AAAAAATATA	100
	TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA	150
15	GTGCTTACCC CTGGGAAGGG GGTATACGGAT GTTGATTTAC TCTTTGGGTA	200
	CGTATT	206

20 (2) INFORMATION FOR SEQ ID :100:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :100:
CGCAACTNTC NCTAAACATC CAGTTTCTA ATNTAATAAA AAATGGCAGT

AATTATCCTC ACCTCTCAGG GAA 73

35 (2) INFORMATION FOR SEQ ID :101:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50
ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT 100
ACTGCC
10 ACTGCC 108

10 (2) INFORMATION FOR SEQ ID :102:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTA TTTTCCAGCT TTGATCTTAN 50
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AACGATNTAT 100
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150
TCAATATAAC ANAAAAAGGN ATTTGCAAA AAGTACAAGT TTTATGTCTN 200
30 CTGTTAACTG 210

(2) INFORMATION FOR SEQ ID :103:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

CGTAGTCGA TTGGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT

50

GTCACCAAAA TTTCTTCCA AAAAAAA

76

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAAA TCTTCATAG AAAGATATTA TCAAAGCTGA

50

AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCCTTAA

100

20

CCGATTGAAT GGTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC

150

AAGTCGCAAG GAACATC

167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC

50

CTCACGGGAC CACCATCATA CAGCAATTG TCATGATCAA AAGAAACATC

100

40

ATTAGTCGTG CCATAACTGT AT

122

(2) INFORMATION FOR SEQ ID :106:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :106:

	GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT	50
15	GGAGGCAACC AGGCCC GTTT CCTCCTTCA AAGTCACCC TCACAGACTC	100
	ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA	150
	GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG	200
20	TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA	250
	AATAA	255

25

(2) INFORMATION FOR SEQ ID :107:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :107:

	GGACGTGAAT TGGTGGAAATA TTTACAAAGA AAACGTTTT CTCAAAACAC	50
	TGTTCATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA	100
40	AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT	150

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT

200

ATACCAAGAN ACANTTATGT GGTAAAT

227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTTNNNN NGCCATACCA TGGTACAATA

50

ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA

100

20

CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAATAGNAAAAA

150

AAAAAAATAA CA

162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCATAA

50

40

AAATAAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC

100

ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCATACTG ATCATTCA

150

(2) INFORMATION FOR SEQ ID :110:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15 ATGTGCCAAG TAAAAAATCA ATTNGTNGCC TTTTCCATT NCGCGGACAC 50
CCATAGGCAC CAAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG 100
AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT 150
20 GCACTCCTTG TTAATAACAA TACACTATAT CA 182

(2) INFORMATION FOR SEQ ID :111:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35 GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTACGTA 50
CNTCAAAACC AATGGTAGAA CATCACATTT CAAACTGCAA ACCA 94

(2) INFORMATION FOR SEQ ID :112:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10	TAGGGCAGTG AACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT	50
	GNTCATTNGT TAAATTTGT TCTAAACCCA TTAGGAAATT GT	92

(2) INFORMATION FOR SEQ ID :113:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25	GATTGTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG	50
	TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG	100
30	ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG	150
	GG	152

(2) INFORMATION FOR SEQ ID :114:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 182 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTTCAGTG 50
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG 100
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA 150
10 TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA 182

10 (2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC 50
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATAACNTGGC 100
AGAAGGAGGC TGAGAAAAGTG GCTCCGTGAA GGNCNCTATAG AGGGCTGATC 150
30 TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT 182

(2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :116:

	GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTC ATAAANTAAC	50
	ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA	100
5	TTTTCGGAAA AGTGTAAAAA AAAACANNCT AGATTCAGT GCAAAATGT	150
	ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA	200
	TGGAAATAAG CTAGCTACGC TCAATGC	227
10	(2) INFORMATION FOR SEQ ID :117:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :117:	
	CGAGAGATTG GTAATGAGGA AGCAATTGG AGGGGNGGAA GCTACAANGA	50
25	NNNNNGGAAT TACAACAATC AGTCTTCAA TTTGGACCC ATGAAGGGAG	100
	GAAATTTGG AGGCAGAACG TCTGGCCCT ATGGCGGTGG AGGCCAATAC	150
	TTGCAAAACC ACGAAACCAG GT	172

30 (2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40	(xi) SEQUENCE DESCRIPTION: SEQ ID :118:	
----	---	--

78

100
150
200
210

AATGATGGAA GCAATTTGG AGGTGGTGG AGCTACAATG ATTTTGGAAAT 50
TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTGGAG 100
5 GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG
AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG
GCAGAAGATT

10

(2) INFORMATION FOR SEQ ID :119:

15
20
25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

50
95

GGTAAACACA AAGAGTTCT GATAGTGTCT GCACAACAGC AAACCAACAT
TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC

25

(2) INFORMATION FOR SEQ ID :120:

30
35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

50
100

GGAGTATTTN AANNTTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA
TACTGCTTCC AATATACTTT AATCCTTTT TTCTCGTTAA ATTTTTTTG

TTGTTCTTCA GTTGAGCTGA GATACTTTA ATTACTTTT ATTAAC TGCT

150

TCCAGAAACC GTAACAGG

168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTAA TCTTCAAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA

50

CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTCN NCTGTTTTC

100

20

AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA

150

ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA

200

25

ATACATACTT CGGTGACNTT ATGCATCATG A

231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT

50

40

AGCTGTTCAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG

100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT 150

GGAATCTTTC TGAAAAGGAT ATGA 174

5 (2) INFORMATION FOR SEQ ID :123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAAATG TTCTGTTATC 50

AACTGNNTTT ATAAAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT 100

20

TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTTGA ATTCTTANGA 150

AACATNNNTNG NNGAATCAAT 170

25 (2) INFORMATION FOR SEQ ID :124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNNTTATAAA 50

AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC 100

40

ATGANGAAAA ANNTCTGCC TTTGAATTCT TANGAAACAT NNTNGNNGAA 150

TCAATNT

157

(2) INFORMATION FOR SEQ ID :125:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15 CAACTTGAAA TACATTATGA TGTCTGATAT GATTAATAT CATTGAGNAT 50
CTTGCAAAACA AAAAAAGCAA AAAATTAAT CTCCATATCA ATCTTAAATT 100
CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT 150
20 GTGTTATTGA AATTGTGTT 169

(2) INFORMATION FOR SEQ ID :126:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35 GTTTNGTTNN NNNNTGTTCC ACCTTTGTT GAATTTAGT TGTTAGGCTG 50
AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTTCTTC 90

(2) INFORMATION FOR SEQ ID :127:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

10	TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG	50
10	AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTCAG CAACTTGACA	100
	TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTT TATGCTAAGT	150
15	AGGAAAACCA	160

(2) INFORMATION FOR SEQ ID :128:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 150 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

30	GCCCACAACT TACATCCTCA TTATTGGCGC CTACAAACTC AACTACGAAC	50
	ACACTCACAG TCGCATCATA ATCTTTGAG GACTTCAAAC TTACTCGGCT	100
	ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC	150

35 (2) INFORMATION FOR SEQ ID :129:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 182 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :129:

	AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTTCCGAAG	50
5	CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTAACG AGTCCCACGA	100
	GAACACACCA GAAATTTGTC ATTGCACCTCA ACCAAAATCG ATATCAGCAA	150
10	TGAAAAAACCC AAAACAGTTA CGANGCTAAT CC	182

(2) INFORMATION FOR SEQ ID :130:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 219 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :130:

	GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGCAA GAGGGTGGTT	50
25	TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC	100
	TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT	150
30	TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCAAAC ATNTTACCGA	200
	TGCTTACTTC AAGAAGAAG	219

(2) INFORMATION FOR SEQ ID :131:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

84

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

	AATAATTCCAT CCACTTATGG AGGAGGGAGGA GAATGTGGAA GAGGTAAAAA	50
5	GCTGGGCACA AGTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT	100
	CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT	150
	AGAACATCGT TAACGGAATC ACAGATATAT C	181

10

(2) INFORMATION FOR SEQ ID :132:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 188 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :132:

	GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT	50
25	GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG	100
	TAGAAGATGN AAACAACCTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG	150
	CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC	188

30

(2) INFORMATION FOR SEQ ID :133:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 190 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

	GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC	50
	TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT	100
5	CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTCAC AGAAGCTCTG	150
	TGACTTGGTT GTGGAAGAAA TCTGAACGTGT TCAAGTTAAC	190

(2) INFORMATION FOR SEQ ID :134:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

	ACATTACCGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC	50
	AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC	100
25	CAGGGTCCAT TTAACTAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT	150
	GTCCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA	200
	TCTGGGCCAG CATTGCCATT ATTGAGTTA TCTAG	235

30

(2) INFORMATION FOR SEQ ID :135:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

86

	GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT	50
	ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACCA CTACAAAATC	100
5	AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG	147

(2) INFORMATION FOR SEQ ID :136:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 171 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

	GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA	50
20	CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG	100
	NTCCCANTGA GTCACGGTGA CTTACCCCTAA ACATCTCAAN NGTNNTCTGA	150
25	CTNAGAAATGC GGAGGGAGATC T	171

(2) INFORMATION FOR SEQ ID :137:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 159 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

	ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT	50
40	TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG	100

150
TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTTGAGTCT

159
GTAAGTAGG

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

50
CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAAC TA AACTACGAC

100
20 NCACTCACAA TCGCTCATAA TCTCTTNAGG ACTTCAAACT NTCTCTNTGA
NCCTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCCNNTGTNC

150
TNCGGGAGAA CTCTCTGTGC TGTACCAAGT

179
25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

50
GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC

100
40 TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG
ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAGA

150

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

(2) INFORMATION FOR SEQ ID :140:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTGTGA 50

CTTATACTGT CTNTGTCAGT TA

72

(2) INFORMATION FOR SEQ ID :141:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30 GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTAA AGTATTNGTT 50

TTAGTACGNA AA

62

35 (2) INFORMATION FOR SEQ ID :142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50
GGTCAGCTTC TCTTCCTTTA TCTTTCTTTC TCCCTTTTTA AGAAAACGAG 100
TTAAGTTAA CAGTTTGCA TTACAGG 127

10 (2) INFORMATION FOR SEQ ID :143:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

25 AATATAAAAG ACAGCAGTTT CACATTCAC ATATTTGAAA AACATTCAA 50
AACCTCTAA TAAGTATTAA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100
GACCACAAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA 150
ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT 198

30 (2) INFORMATION FOR SEQ ID :144:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

 GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

	AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNNTAC CTAAAGCTTG	100
	TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG	150
5	AAACTGCTTT GTATCTGCTT TGNA	174

(2) INFORMATION FOR SEQ ID :145:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 156 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :145:

	GAGAAATAGT ACTTTAAAAT AAAACTAACCA TGTTTGATC AGCTTGAAAT	50
20	AAGATTCTATA AAATGTACCT TTTTGATTG TTTGTTCTN GAGTTTCGA	100
	TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA	150
25	TTTG	156

(2) INFORMATION FOR SEQ ID :146:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 151 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :146:

	AAGATTCCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG	50
40	CTTGGAAATT GGCTGTTTG TTAAATATA TCTTTAGTG TGCTTTAAAG	100

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT

150

T

151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNAG TACCAAAC

50

20 CAGGTAANNT GGTTGATCT GATCGATTTG GCTGCATACT TTCGGTACGT

100

ATAACATTCT AACTTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG

150

TAAAATTTA AAAGTTAAAG TACTAGC

177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCCNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT

50

40 TGGAAATTGG CTGTTTGTT AAAATATATC TTTTAGTGTG CTTTAAAGTA

100

GATAGTATAAC TTTACATTAA TAAAAAAAT CAAATTTGT TCTTTAAT

148

(2) INFORMATION FOR SEQ ID :149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCCNNNN	NTGGNATTGA	ATGTTACCTG	TGCCAGAATT	AGAAAAGGGG	50	
15	GTTGGAAATT	GGCTGTTTG	TTAAAATATA	TCTTTAGTG	TGCTTTAAAG	100
	TAGATAGTAT	ACTTACATT	TATAAAAAAA	ATCAAATTTT	GTTCTTTATT	150
20	TTGTGTGTGC	CTGTGATGTT	TTCTAGAGT	GAATTATAGT	ATTGACGTGA	200
	ATCC					204

(2) INFORMATION FOR SEQ ID :150:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35	AACATCGAGG	TCGTAAACCC	TATTGTTGAT	ATGGATCTCT	ATGAATAGGA	50
	TTGCGCTGTT	ATCTCTAGGG	AACCTCACCG	TTGGCAAGTT	ATT	93

(2) INFORMATION FOR SEQ ID :151:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

10	AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT	50
	ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC	100
	CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAAC CAGGAAGGTG	150
15	T	151

(2) INFORMATION FOR SEQ ID :152:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 109 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

30	TCTGAGAGGA ATACTNNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCT	50
	CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA	100
	TGTAGCCTC	109

35 (2) INFORMATION FOR SEQ ID :153:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 136 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50
 TCCAATCCTT TTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100
 AGGAAAAGGG GAAAAAAACC CATAATGGGC CTAAAAA 136

10 (2) INFORMATION FOR SEQ ID :154:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

 CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50
 CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100
25 TCAAGATGAG TATACGCATC TATCATTGGA ATTGTGTCAT TAATTGTTAG 150
 GGCCTCATTG 160

30 (2) INFORMATION FOR SEQ ID :155:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

 ACCAGTNNNN NNNNGTCAA TAGGGAATA TAATTCGATC TCTCGAATCA 50

95

	ACTCTCTGGG TCAGCTTCT NCTTNTCTTC TATCTTNCT TNTCTCCTTT	100
	TTTTAAGAAA AACGAGTTAA GTCTAACAG TTCTCGCATT ACAGGGCTTGT	150
5	GACTTCATGC TTACTGTAAA GTGGAAGTTG AGATATTTA A	191

(2) INFORMATION FOR SEQ ID :156:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 139 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

	CAACTGAACG CTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN	50
20	TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT	100
	GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCAGTG	139

25 (2) INFORMATION FOR SEQ ID :157:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 172 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :157:

	GGTACAGAGC ACTCTGTACC AACACACAGA ATTACTGTT CTGCAAATGA	50
	CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT	100
40	TCTTTTGTAA ACAAGATACA ACATTTAACCA GTTATTAAAT GTAATCCTGA	150

AGCACCCGCA AATTACCTT TG

172

(2) INFORMATION FOR SEQ ID :158:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15

GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT

50

CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG

93

(2) INFORMATION FOR SEQ ID :159:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30

GNATTTTTT ATTGATATAT CATACTGTA CAAACATTG GGAGTNCANG

50

TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC

100

35

CA

102

(2) INFORMATION FOR SEQ ID :160:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :160:

	GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA	50
10	TAGAAGCAAT AANNNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT	100
	ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT	150
	ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTGTA	200
15	GCGGA	205

(2) INFORMATION FOR SEQ ID :161:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

30	AACTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNNGNNAA	50
	AGTTGTTTC CATATAAAA ANNNNNNTGA TTTTAAAAAA ACTAANNAAC	100
	TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA	150

35

(2) INFORMATION FOR SEQ ID :162:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :162:

TATTCAAAAG AAAAACATGG GTAAAAATGA TAGTGTAAA TCTTGGCTCT

50

5

GTGTACATAG ATAGATACCT GTTACAG

77

(2) INFORMATION FOR SEQ ID :163:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCCACTTC TTGCTCTTAA TCCTCATCTT

50

TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT

100

25

AACTTAGCAG CACAACACGG TTCTTTATC AAGGCGTNAT CATCATTCT

150

CAAAC TGACA TGCTACAGAA ATGTCTTCCA AA

182

(2) INFORMATION FOR SEQ ID :164:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA

50

TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC

100

99

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150

CAGATTTCACA GACATTTGCA AAACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT 50

GAGACATATA TACCACCCAA GTTTAACAC CATATCCCAT CGGCTGTTAG 100

20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTCC AAACACATAG 50

GATCCCATCT CAGGAGCAGG ACCAGTGTTC AGCTAGATTA AACTTCGCTG 100

40 GTGATCTTGT TGATGCATAT AAAGTAATCT GGCAATATAG GTTAAATTCA 150

AGATGTTATG GCAGAAGTGA CTTGTTTGCA TCAACAAGCA TTG 193

100

(2) INFORMATION FOR SEQ ID :167:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :167:

20	GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG	50
15	GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT	100
	GAGCCAGTCT GAATCTCTGT GAAGATGCC CAGTGGAGGT GGCTGAAGAT	150
	TAAATGGACA GTTTATAAAG TGTTCTGG> GCCGA	185

20

(2) INFORMATION FOR SEQ ID :168:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :168:

35	GGACAACACA GCACCCATCC ACTACCCATT CAGAATTAT ATAGAATATG	50
	TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG	100
	ATTTCTAGT CTATTATTT GTGTACAGAT CCTCTAACCA CTTAGAAATA	150
	ATTTTTAAAA ATA	163

40

(2) INFORMATION FOR SEQ ID :169:

101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10 AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50
GCAAAGGGTG AACATGTTT CAACCCTTA ACTTTTACG GTGTTGAAG 100
15 ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTG 150
CAGATTTACA ATTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC 200
CT 202

20

(2) INFORMATION FOR SEQ ID :170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAAACTGG CTTGCTGGC ACCCAGGGAC AGTAGCTGTT 50
35 TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTT CCCCCACCCC 100
ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150
GGTGCCCAGG GCTGTAAA 168

40

(2) INFORMATION FOR SEQ ID :171:

102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA

50

GCAATTATG ACACATTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC

100

15

TTCCCGAAAT GATCAGGACT GATTCACTTC CTGAAATTNN CNGT

144

(2) INFORMATION FOR SEQ ID :172:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :172:

30

ACCCACAGNN NNNACCTAGA GGCCCAGCGC CCAGAGAGGC ACGTAGAAAT

50

GGGGACAGCA CGTTTATAGA CCACCAAGAAA TTGAAGAGGA A

91

(2) INFORMATION FOR SEQ ID :173:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

	GATTTTTAA TGGGTNGCCT CTTTAGCTT GGAATATTAC GTTTACTTA	50
5	ATCCAAGTCT AGGCCTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT	100
	GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTT GGTGTGATTA	150
	CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTGGCA GAAGTTAAAA	200
10	TGGA	204

(2) INFORMATION FOR SEQ ID :174:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 241 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25	GTAAATTCA CTACATCTT TNNTNTGACT TTCATGCATT TCTCATAACAT	50
	TNNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA	100
	ACGAAAGGCG GTTCAATTCA TCAACTGAA ATGACTATTT ATTTTNAGG	150
30	ATTTTTAGG GGAAGAGTAC CCATTCGTT TATAAAAACA GATGACAAAT	200
	TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G	241

(2) INFORMATION FOR SEQ ID :175:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :175:

	GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT	50
5	TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT	100
	AACAAACCCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC	150
10	TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT	200
	TTGGCCCTTT T	211

(2) INFORMATION FOR SEQ ID :176:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 252 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25	AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG	50
	NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN	100
30	TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA	150
	AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTCT GACCTATGAT	200
	AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA	250
35	AT	252

(2) INFORMATION FOR SEQ ID :177:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 279 base pairs	
	(B) TYPE: nucleic acid	

105

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

	GGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA	50
10	GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCCGAG	100
	TTGCAGCCAA TCTTCTCAAA GCAAACCGAC TTCTAACAA CTNTCTACAT	150
	CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTAAC ACCACAATCA	200
15	TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGATGTTCT GAGTCTNTCC	250
	ATCTGAAGAT ACCAGCTTCA AATACTAAT	279

20 (2) INFORMATION FOR SEQ ID :178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :178:

	TATGCCCTGA AATGAAACCT CTAAGTTGA CAAAATACCC AAAAAACAG	50
	ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTG GTGGGTGGTC	100
35	GTTCTCAATT TATAAAANAA TAAATGACTT TAAAGGAGAA ATAAATTAT	150
	GTCAGGA	157

40 (2) INFORMATION FOR SEQ ID :179:

(i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10

GATAATGCAA CTTTGACAG GAAAGCGCGA TTTTACTAT

39

(2) INFORMATION FOR SEQ ID :180:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

25

GCAAACCTCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG

50

GACTTAAACT CTACTACACT AATACTTTT GATGACTTCT AACAAAGCCTC

100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG

150

30

TACCAACA

157

(2) INFORMATION FOR SEQ ID :181:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

	CCATCCAGGC CAAATAAGCN CGGGCTATGC CCNTGTATTG GATTGCCACA	50
	CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC	100
5	ATTCTGGTAA AACTGGAAG ATGACCCCTAA ATTTGAAGT TGATGATGTG	150
	CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT	195

(2) INFORMATION FOR SEQ ID :182:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20 CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT 50
GTTTGTCCCTT CAAATGGGAC AATTTGAGGA ATGCTTTAGG CAGAGGACTC 100
25 AGATGACAGA GCGCCAACCA CCCACAATAG AAACCTGCTC ATCACA 146

(2) INFORMATION FOR SEQ ID :183:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :183:

40 TAGAGGAATA GGGNNNGNGA CGCCCCNAGT TGTAGGGACG GACGGAGGAC 50

(2) INFORMATION FOR SEQ ID :184:

108

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10 ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50
AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCCG AACAGGAAGG 100
15 CCAGGATCCA TTTACCACAG AGGCAGGATC TCCACGCCAA CCCCCAAAGAT 150
GTCCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA 200
TCTGGGCCAG CATGCCTCAT CTGATTTCATC TCGCTTCCAT CAATGNGT 248
20

(2) INFORMATION FOR SEQ ID :185:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :185:

60 AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50
75 ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT CGCGAGAGAA ACACCCTTG 100
80 AACGTGGCTT TCT 113

(2) INFORMATION FOR SEQ ID :186:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs

109

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

10	GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTCC CAGGATCCCG	50
15	ATGTCGTCA ATCACTCCGAA CATGACCCTT TTTCTTCCA ACGATCAACC	100
20	ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC	148

15 (2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :187:

30	TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG	50
35	TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA	100
40	GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT	150
45	AATTAAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC	200
50	TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC	248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG	TGCAGCACTG	GCCAACACCA	GGGTTTACTG	AATCATTCA	50
GTTTAATACA	TAAGTGTCCA	ATAATAATGT	CAACCCTCCC	TCGCCACAGC	100
10 CAATAATTTG	TCCTCACTGA	GTTGGCAACA	AGTGACTGCT	GTGACT	146

(2) INFORMATION FOR SEQ ID :189:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 81 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25	ATTTACCACA	ACGGACGATT	TCCACACCAA	CCCCAAAAAT	GTCCCCTATG	50
	ACGACGAAAT	GTGTATTTGA	AACAGCTCTG	A		81

(2) INFORMATION FOR SEQ ID :190:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 136 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

	AAGTACAGCA	TCCTGCTGCA	AAAATGATTG	TAATGNCTTC	TCATATGCAA	50
--	------------	------------	------------	------------	------------	----

111

GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTG TGAGCTTCCT 100

GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50

20 ATGGGGCATA CGAGTAATAT GTACATATCA AACAAATCAAT TGCCTCCTGA 100

AATCAAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA 150

CA 152

25 (2) INFORMATION FOR SEQ ID :192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTGAT TGCCTAGTAA GGTAAAGACG ATTTTATAGA 50

40 ATNAAGGTGA TTCCCT 65

(2) INFORMATION FOR SEQ ID :193:

112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10	AGGACCCAAA CTACCTTATT GCATTTGAAG TTTTACTTAT NCTATTATAA	50
	TCTAAGAGCC CACCCAACAA GGCAC TACAC ATAGATGCTC ACAC TCTATA	100
15	GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG	150
	CTGTCAATGA CTAGGGAAAG CTTTTAAGA CCCAGCGATC ATGCAATGGC	200
	TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA	249

20

(2) INFORMATION FOR SEQ ID :194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :194:

25	GGAAAGGGTG CCTCATCCC GCAACCTATC CTTGTGGGNG ATGATCACTG	50
	TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC	100
	GCTGCATATG TGACTGTCAT GAGATCCTAC TAGATGATCC TGACTAGAAT	150
	GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT	194

40

(2) INFORMATION FOR SEQ ID :195:

113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10 GTGATTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50
TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA 100
15 CATCCTTTNA TATGNNCNGN A 121

(2) INFORMATION FOR SEQ ID :196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :196:

30 GGGCTTCNNN NNNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC 50
CATTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100
AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA 150
35 TTGTGACCAAC AAGTCTTGTT TCTTG 175

(2) INFORMATION FOR SEQ ID :197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

	ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG	50
	AATCAGAGGT ATCAATGAAA TGAGCCAAA GGTTCGAAAG CTCGCAACTT	100
10	CTTCACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT	150
	ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA	200
15	AATGACTAAT CTACAAGCNT GTTATGCAAA ATAAATAAGA AACGACTTGC	250
	TTACAGATGC NTTTTAATTG TGG	273

20 (2) INFORMATION FOR SEQ ID :198:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 56 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

30	GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT	50
	GNATATA	56

35 (2) INFORMATION FOR SEQ ID :199:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 132 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50
GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTAAG CAACTCTTAC 100
CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

10 (2) INFORMATION FOR SEQ ID :200:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

25 AAACTTTTN GCACCTTACAC AGACGAGACT TCACTGCNTG AGGATCATAAC 50
GACATTTCAA TCGNACACAA ANTTAAAAAA TAAAACAAAT TTTAAAAAAC 100
CATNTTGAAT TTCCCTTAAAAA TTATTCCAAT ACTTTCCAAC TTAAAATTCA 150
GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200
30 CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN 250
TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

35 (2) INFORMATION FOR SEQ ID :201:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :201:

	CCTGACACCA ATTCGCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA	50
5	AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTNT	100
	CTTGNT	106

(2) INFORMATION FOR SEQ ID :202:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20	CTTTGGAAAA CAAACATTN TTATTACTGA AATAGCAAAA ATCATTCTAC	50
	ACTCCTCCTA AGCATGTTCA ATTAGCATAAC ATTCCAACAA TGCATGAAAA	100
25	AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCCTAAGT GTTTGCTAAT	150
	TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA	200
	CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT	250
30	CATTACTCTA ACTGTTAAC	270

(2) INFORMATION FOR SEQ ID :203:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

	AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA	50
5	AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA	100
	ATAATGACAT ATGAGAATT TTTATTACAT ATTAAGACTG ATTTTACTT	150
10	TACAAAANNG NAATTGCAA TTA	173

(2) INFORMATION FOR SEQ ID :204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

	CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN	50
25	ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT	100
	CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT	150
30	CATTAACATT ANTT	164

(2) INFORMATION FOR SEQ ID :205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100

20 TGGGGTTAGN TGTTCNA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTAA 50

TAAAAAATACC TCTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCG 100

40 AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150
GCTATGCATA ATACCCTCAC 170

119

(2) INFORMATION FOR SEQ ID :208:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :208:

15	TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAC CCTAAGACAA	50
15	CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATT	100
	TTTCTCGGGG AAGTAACCCT GCCTTTGAA	129

20

(2) INFORMATION FOR SEQ ID :209:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :209:

35	CTTGGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG	50
35	GATCCTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT	100
35	CCAAATTTG GCTCCAGAGT CATTCTGAA NNTCTACACT TANGGNCTTN	150
	AGCNGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT	190

40

(2) INFORMATION FOR SEQ ID :210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs

120

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

10	TCATTGAGTC ATCCTTTTG CCTGCTGCTG TAAGGTTTT TTTCTTCTAG	50
	TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT	100
	GATGCAGAAC TGTTTCATAT CTAGAAATG	129

15 (2) INFORMATION FOR SEQ ID :211:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

	CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG	50
30	CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG	100
	AAATGGAANC NNNGNGTTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT	150
	GG	152

35 (2) INFORMATION FOR SEQ ID :212:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 186 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

121

(xi) SEQUENCE DESCRIPTION: SEQ ID :212:

	CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG	50
5	TCGAAAGATG AAAACAACTA AGTTCATAAC CCCCTGCCCG CCATTGACCT	100
	CCCTTNAAA ANCAGAGACCA AGACTCCATC ACTGGTTTCG AATTTACATC	150
10	NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT	186

(2) INFORMATION FOR SEQ ID :213:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :213:

	CTTAAATGCC TGTTGTATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA	50
25	CCTTTCTCTA AAATTCCCTT CCTTTGCCTC CTCCCTCTAAC TTTTCCCTCT	100
	TTCNCGCTTT TCCTCAGGCT TTGNTTTCC TCATGCTTTG CTTCACTCTA	150
30	TT	152

(2) INFORMATION FOR SEQ ID :214:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 290 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

	TCTTCAGGAG AAGGGGCACC ACTGCTTAA AAAACAATAC TCCNTTATAG	50
	ACTTGAACAT TTGCAGACAT TATGATCTG CTTCCAACTC CCACCGTATG	100
5	TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC	150
	ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT	200
	GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT	250
10	ATTATTCAAT AGTGGAAATG ATGACTACAG CTATACCTCA	290

(2) INFORMATION FOR SEQ ID :215:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 273 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25	GTTTCTTCCA GTACATCCAA GTTTAAAATT ATTAGCGAAA TGGTCCATGT	50
	TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGGAAAGATCT	100
	GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCAATGATG TAACAGGTCC	150
30	TGGGCCTCAC TTTACCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC	200
	TTACCTACCT CAGAGGGATT TGCAGAAGCAA ACTGTTAACATC TTCGAAAACG	250
35	ACCATTTACT TTTAGGATAT CAA	273

(2) INFORMATION FOR SEQ ID :216:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 118 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT	AGGGAGAAC	AATGTTCTA	CATATTATGG	GTAGTGAGAA	50
CATTATCTGT	ATAACAGGGA	ACTGTGATTA	TTTAAAATTA	TGCAGAACTT	100
10	ATTTCATCTG	TGCTTTAG			118

(2) INFORMATION FOR SEQ ID :217:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 197 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25	GAGGCTGGTG	GCGAGGGACT	TGTGGAGGAT	AACAAGAAGA	AAACAAGTCT	50
	ATCACTAATG	ACTTATTTTA	CTTAGTTCC	ATTCACGAAA	CCCTTTAAA	100
	TACAAGGCAA	CATTTCACA	GCTGAAAAAT	TACAAC TAAA	NGNNNTGATT	150
30	TACCAACAAA	AGCAATAGAT	GTAGTTATGT	ATAATCTATA	GATAATA	197

(2) INFORMATION FOR SEQ ID :218:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

	CTCGCGAGCA CTCGTCCGAG AGGTCCCATA CNNNNNNNNCC CAAGCCCCTC	50
5	AAGGGCCTT GCCAATCTNG TCATTTATG CCAAGTCCTC TAAAACGCAC	100
	TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC	150
	TATTTTAGGC TNCGAGGTCA AAATAAA	177

10

(2) INFORMATION FOR SEQ ID :219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :219:

	GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA	50
25	GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG	100
	TNGGTNTCAG GGCTGGAC	118

30

(2) INFORMATION FOR SEQ ID :220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :220:

	GAGAGCCCAAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTT	50
--	--	----

125

	ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAACGTGA	100
	CTTGGACCAAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCCGCAT	150
5	TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN	200
	NGGTTGGNGG AAATATNNNTT TAATCTCAGG CCA	233

(2) INFORMATION FOR SEQ ID :221:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20 GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA 50
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAACCTG 200
TGAGCCTGCC ATTCTTTTTT ACGTGTTAAT CAATT 235

30 (2) INFORMATION FOR SEQ ID :222:
(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

	GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG	50
	CCTTAGGAAT TGANTGAGGA CTTAAATTTC CCCNGAGGGA GAGNAGTGGA	100
5	G	101

(2) INFORMATION FOR SEQ ID :223:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

	ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC	50
20	ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT	100
	TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT	150
25	TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACCA CCGACAATTA	200
	ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC	250
30	CATTCTTGAG ATACCAAGCTT C	271

(2) INFORMATION FOR SEQ ID :224:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

	AGTATTATTT ACTNGGTCA CTGGGAACCT TAATGTGATT TATTTGACA	50
	ATTACTGTGG CACATGTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA	100
5	T	101

(2) INFORMATION FOR SEQ ID :225:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 141 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :225:

	TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATAACAGGN NNTGTACCGT	50
20	AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA	100
	GACCCTGTTA ANTTGGTGA AAATAACTTT CCANATTCA A	141

25 (2) INFORMATION FOR SEQ ID :226:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :226:

	ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG	50
40	TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTG	100
	TTCTGTTATG TGCAAAGTAG ATTATTCAT ATTTACTTGG TATGGAAAGC	150

128

AGAGTACAGG CTCATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200

AAAANGCTGT TNNAAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNNGTGG 50

20 TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100

CAGTTAACCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150

TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCNCG 200

25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

40 TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50

ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTT TTTTAAATG GTAAAACCCC

150

TTTTTACTGG NCNTTCCAGA ANCTTACAG

179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCACAAGT TATTGTAGCA GTGAAACAAT

50

GAGGGCATAAC ACTATATNGA AAAAAAAACC TCCTCCCTNA TTCTCACGCC

100

20

AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA

150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA

184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTC

50

TTTTTAGGTT TAGAATTGAGCAAGTAT TGNTATGGTG AGCTGTTTA

100

40

GTGCAAACAT TGTTGAGTAT GTTGTCAAAC GTCTAAAAAA

140

130

(2) INFORMATION FOR SEQ ID :231:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTNT NNGTTGGGG CCGTCCCGCT 50
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNNG ACGAAAAAGT CGCTGGNGNN 100
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150
GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

(2) INFORMATION FOR SEQ ID :232:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC 50
35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATT TATANCTCN 150
NCGAAACAC ACTTATCCCC ACCTTGGTCT ATTCAATNACC CGGATNGAGG 200
40 GCAACCANGG 210

(2) INFORMATION FOR SEQ ID :233:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :233:

	ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTATAC	50
15	AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC	100
	CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG	150
20	ACTNTCTNAC NTTCAAACNA NTATTNCACG TAAAAAACAT CACAGTGCAG	200
	AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG	247

(2) INFORMATION FOR SEQ ID :234:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :234:

35	AAACACCAAA NAAANNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT	50
	GTGGACATTG GAATGTTAC TGTTATTCTG TGTAAGAAAA CAACTNACAA	100
40	AAAAGAAAAA TGGNCAACAA AATTGTTCC CGGCNAGGCT GNAGGAAACC	150
	NGGGGGAAAN TGCCNGGGC	169

132

(2) INFORMATION FOR SEQ ID :235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA

50

15

G

51

(2) INFORMATION FOR SEQ ID :236:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAA TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC

50

30

TCAAACTTT TTAGGAAAGC CAGATTAAGA GCAGACGTAC CTAAATNCAA

100

A

101

35

(2) INFORMATION FOR SEQ ID :237:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :237:

	CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG	50
5	ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA	100
	CAGTTTCCA GCAGTTTCG TATTTNTTT TATTTACGAA TGCCATACTC	150
10	TGTTTT	156

(2) INFORMATION FOR SEQ ID :238:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 148 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :238:

	GCAGNCTAAT TGTGAATCTA AGAAACTACT CATAGACATC CCACCCCTAAT	50
25	GATTTTACCT NNAACNTTG TCCTTCATCA TAGAACCTA GCAACATCCA	100
	CCTCCTGTAG CACGAAACGA ATCAAACAAAC CCCCTGGATA ACCTCTCA	148

30 (2) INFORMATION FOR SEQ ID :239:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 258 base pairs
	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :239:

	GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA	50
--	--	----

134

	AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA	100
	AGCACAAAAAT CAGCCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA	150
5	TCAACTAAGC TCAAGATTT ATTCAAGATTT GACTAGTTT TCCACTAAGG	200
	CCCTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA	250
	TCTTCTCT	258

10

(2) INFORMATION FOR SEQ ID :240:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 377 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

	GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA	50
25	CAAACCAGTG ATTCCCCCTTC CTCAGATACT GGGACTAACCA GCTTCACCTG	100
	GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACCA CATTAAAAA	150
	CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT	200
30	TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAACG TTTGCCATTG	250
	CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC	300
35	AAGGGTNAAC NTNTTTNNAA ANNNGCCNAA NCNNGATTT GNACNCCTT	350
	TNNCATTGGC ATTNANTGAA AAAAGTT	377

40

(2) INFORMATION FOR SEQ ID :241:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 114 base pairs	

135

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

10	GGNGCACTGN TCCGAGAGCT TTTTTNCTG AAGAATAGCA TCTTTAATGA	50
10	GTGTNCTAAT CCTTGTTCATC TGAAGTTTG AAATATATTT CCCAGGGTCA	100
	GAACAATACA GAGA	114

15 (2) INFORMATION FOR SEQ ID :242:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 122 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

	CTCAAAATNC TGTGACAAAT TTNNNNNGTC AAGTTGTTNN CCATTAAAAA	50
30	GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCACGNAAAAA	100
	AAAAAAANCNA AAGNGGGCCC CC	122

(2) INFORMATION FOR SEQ ID :243:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 171 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

	GAGAATGGGA AGCCTCATTG TGGGGACAAG AACCTGTACA AGGATTGTG	50
5	ATGAACTTTT CCAATGGGA AATTATAGAC ATCTTCAAGC CAGTGCAC	100
	NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA	150
	TTGGNGATGC TCATCCAAAC C	171
10		

(2) INFORMATION FOR SEQ ID :244:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 235 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :244:	
	AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT	50
25	TAAGAGAAAT ACAGAGTGTG TGGTATNTGA GAGAAAAAAA GTAAAAACAG	100
	GACTTTCAAC TTAATCCAGA CTTCCTAACCA GTGTTTACAT GTGAGGGAAA	150
	CTCCTTTAAG TAATGCGTAG TGTTTATTT TTACCATCAT TGGNGACAAA	200
30	AAAAACAAAA ACATAAACAT CTNANGTGAATATA	235

(2) INFORMATION FOR SEQ ID :245:

35		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

137

(xi) SEQUENCE DESCRIPTION: SEQ ID :245:

	GGCCTAGCCT GCCATACCCCT TACGAGCAGG CTCAGTGATT AGACTTGAG	50
5	TCTAAGTTAA AAACGCCCTG CCCCCCTCTC GCAGGCCACC TACACCGTNN	100
	TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCCTGC	150
10	NTNTACNTCT AACCTAAACA TNACNGCGGC CACCTACTCA TGCCCTANTG	200
	CAGCNCACCC T	211

(2) INFORMATION FOR SEQ ID :246:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 194 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25	GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA	50
	AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT	100
	ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT	150
30	GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA	194

(2) INFORMATION FOR SEQ ID :247:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 249 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

	GCCCCCTCAA	GGGCATCCTG	GGCTACACTG	AGCACCAGGT	GGTCTCCTCT	50
5	GACTTCAACA	GCGACACCCA	CTCCTCCACC	TGACGCTGGG	GCTGGCATTG	100
	CCCTCAACGA	CCACTTTGTC	AAGCTCATTT	CCTGGTATGA	CAACGAATT	150
10	GCTACAGCAA	CAGGGTGTGG	ACCTCATGGC	CCACATGGCC	TCCAAGGTAA	200
	GCCCCCTGGAC	CACCAGCCCC	AGCAAGGCAC	AAGAGGAAGG	AGAGACCT	249

(2) INFORMATION FOR SEQ ID :248:

15	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 248 base pairs	(B) TYPE: nucleic acid	(C) STRANDEDNESS: double	(D) TOPOLOGY: linear	
20					

(xi) SEQUENCE DESCRIPTION: SEQ ID :248:

25	GCCCCCTCAA	GGGCATCCTG	GGCTACACTG	AGCACCAGGT	GGTCTCCTCT	50
	GACTTCAACA	GCGACACCCA	CTCCTCCACC	TGACGCTGGG	GCTGGCATTG	100
	CCCTCAACGA	CCACTTTGTC	AAGCTCATTT	CCTGGTATGA	CAACGAATT	150
30	GCTACAGCAA	CAGGGTGTGG	ACCTCATGGC	CCACATGGCC	TCCAAGGTAA	200
	GCCCCCTGGAC	CACCAGCCCC	AGCAAGGCAC	AAGAGGAAGG	AGAGACCC	248

(2) INFORMATION FOR SEQ ID :249:

	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 82 base pairs	(B) TYPE: nucleic acid	(C) STRANDEDNESS: double	(D) TOPOLOGY: linear	
40					

(xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5 GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCGCGTTG 50
GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

(2) INFORMATION FOR SEQ ID :250:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50
TNTTGCAAAT CCAGATTGT TGNCATTACT GATGGGCGCC TGAAACCAGN 100
GAGAGATGCA CAAGATTTAC AGGCC 125
25

(2) INFORMATION FOR SEQ ID :251:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :251:
GGCCCAGAGG TCCTTACTC TTACGGNACA CCTTAGCCAC ATTACACAGGG 50

40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTCAAA AGCGCGTTT 100
TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

(2) INFORMATION FOR SEQ ID :252:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :252:

20	GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA	50
15	AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT	100
	TTCCTTGGC ATCTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT	150
	ATAAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTT	200
20	ATGNGATAAT ATCAGC	216

(2) INFORMATION FOR SEQ ID :253:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :253:

35	GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAATT	50
	ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTCCTT CCAAAGAAGN	100
	TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA	150
40	TANATACNGC TTCATNCGTT GGGACCATT AAAAGTAATA TAATNAGCTT	200

TTTTCAGAAG GATCTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT

249

(2) INFORMATION FOR SEQ ID :254:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15 GACCCCATTCA TATATTATNC GTNNNGCGAT TTTTAGCCA CCCTGAAGTT 50
ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCCTNG 100
GAAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG 150
20 CTCCCTGGGN TTCTTG 166

(2) INFORMATION FOR SEQ ID :255:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35 CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTCAA GAGCATCTGG 50
AACAAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA 100
AGATTTGCTC GCTGAGAAAG TCCTTGTGGG AAATCGAAGT TGAGGACTAC 150
40 TTTCAGAATT TGCTCGCTAC ACTACTTGA GGATGCTACT CCCGAGCCCC 200

142

CTTCTNTTGT NACAGACAGC AGA

223

(2) INFORMATION FOR SEQ ID :256:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15	GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT	50
	TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC	100
	TCTCGAGACT ATAATCCATA TAACTATTAA GATAGGCATCA GTCCCTTCAA	150
20	CAAGTCTGCC CTCAAGGAAG CCATGTTGA TGATGATGCT GACCAGTTTC	200
	CTGACGATCT TTCCCTAGAT CATTCTGACC TGGTAGAG TTGTTGAAGG	250
25	AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC	292

(2) INFORMATION FOR SEQ ID :257:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :257:

	AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT	50
40	AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG	100

143

	ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT	150
	GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCCTGACGA	200
5	TCTTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT	238

(2) INFORMATION FOR SEQ ID :258:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 137 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :258:

20	GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA	50
	GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG	100
	AACCGGCTCC AAGCATTCTG CACAGCACTA ATTTAAA	137

25 (2) INFORMATION FOR SEQ ID :259:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 241 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :259:

	GCGCGACTTT TAAGGGATT GCNGTGATGC CTGTTGACCC AGTGCCTTCC	50
40	TAGCCGGGAA GGGGCTCGGC TGGAGTGNNA AGGCTCAGAA AAATTCGCG	100
	AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT	150

144

TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTT CGTGTACAT 200

CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTC CNGTGATGCC TGTTGACCCA GTGCCTTCCT 50

20 AGCCGGGAA GGGGCTCGGC TGGAGTGNNA AAGGCTCAGA AAAATTGCG 100
AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

TTTTGGACAG GTGGGGCGGT GACCTTGGTA TGTATTTTC GTGTACATC 200

25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 239 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

40 GGATCTTC GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50
CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCCTACT 100

145

	ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC	150
	ACTTCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT	200
5	GATCCCTGGA TAAACAGGAT CATTCAAAG NNGTTTATA	239

(2) INFORMATION FOR SEQ ID :262:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 143 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

	GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTTGTAA AACAGCCATT	50
20	GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG	100
	TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA	143

25 (2) INFORMATION FOR SEQ ID :263:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 246 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :263:

	GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCTGTAA TACCTCCTCC	50
	TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC	100
40	TAAAAAAAAA TAGCAATCCA GATAGGCTTC GATTCCCGT GACACTCTGA	150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200

TTGGAACCTT TAGCACAGAT TTGTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid

- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50

20 CTGTGTTAAA TCGTATGCTT TTTAAAGGTA TTTAAAGATT CAACTAGCTT 100

TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTGG 150

ACCTGATCTT GATGTTCTGC TGTTGTNAGT CTTGAAGAGC GTATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50

40 TGCTGAGCCC CCACAGAACT TAATGCCCA ATCTCAGTCT GGTACTGGTA 100

AAACAGCTGC CTTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCC CTCACACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAAATATGT TTCTTCCTT TGAGAATTCA CAAAANGGG 50

TCAAAACAA AGCAATGCTG AAAGCGAACCA TCCATTTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCA 100

40 TCCCAAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150
AGGGTGGAGG CAGATGTCT 169

148

(2) INFORMATION FOR SEQ ID :268:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAACGGGGGG CTGACTGCAG	50
15 GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG	100
CACTGCCAGC AGAAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT	150
20 ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAAACA AGTGCTGCCT	200

20

(2) INFORMATION FOR SEQ ID :269:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG	50
35 ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTG AACAAATTAC	100
TCCACTATAT TAATATTAC TACACCACTT ATTCTTCTT GAATTGTAAA	150
CACTAAGTGT AGT	163

40

(2) INFORMATION FOR SEQ ID :270:

149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :270:

10

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG	50
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA	100
CCACTTATTC TTTCT	115

15

(2) INFORMATION FOR SEQ ID :271:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :271:

30

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA	50
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN	100
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC	150
TGCAGAAATN CCTATGTGAC TCTTATAA	178

35

(2) INFORMATION FOR SEQ ID :272:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

10	CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA	50
	GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN	100
10	NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC	150
	TGCAGAAATN CCTATGTGAC TCTTATAA	178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

30	CTCTAGTAAA AATGTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACAA	50
	AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG	100
30	CTGGTTTTA CTCCAGGAAA ATCGAGGTGA ACATC	135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :274:

	TGTCGAGGAG AAGAAACAC TTGATAACAC CCCGCGACAT CGTGGGGCTG	50
5	CTTGTACAN GAAAGCACCA TGTCGCAAT GGATTGCTGC AGGTGCTGCC	100
	GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA	150
10	TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTGTCCCT CTTCCCTCAT	200
	GACATAGGTG AGCAGTTCC AGTCCCACTC C	231

(2) INFORMATION FOR SEQ ID :275:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 170 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25	TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC	50
	TCTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA	100
30	GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNN	150
	NCGTNCCAC CATTGATTGA	170

(2) INFORMATION FOR SEQ ID :276:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 315 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

152

(xi) SEQUENCE DESCRIPTION: SEQ ID :276:

	ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA	50
5	ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG	100
	AAGGCAGGAGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC	150
10	CTGAGGGAAA CTAATCTGGA TTCACTCCCT CTGGTTGATA CCCACTCAAA	200
	AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA	250
	ACGAAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT	300
15	AGCGTAGCAT ATTNA	315

(2) INFORMATION FOR SEQ ID :277:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 209 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :277:

	ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTGAGA TTTCACAGC	50
30	AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC	100
	ATAGTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT	150
35	AGCAGAAATA GGCCCTTCG TGNGCTGTT C TATTTNCTCC GATNGTAGAT	200
	ATAGTAATC	209

(2) INFORMATION FOR SEQ ID :278:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

10	AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC	50
	TGCTGTTAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTA	100
	GAGTCTT	107

15 (2) INFORMATION FOR SEQ ID :279:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 276 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

30	ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTCAG TAGGAGAAC	50
	CAGTGCAATA GGCTCCAAAA ATGGCTTTA AGACCTTTGG NGGGGCAGTT	100
	ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG	150
	TAGAGCAGCT AGCTTCCTT TCTATAANNA TAGGGAAAGC TCTCTCCATC	200
35	GTCCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCCNCT ATAAGTGCAC	250
	AAAGGGAAA CACTGATTC AAGCTT	276

40 (2) INFORMATION FOR SEQ ID :280:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 185 base pairs

154

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

10	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
15	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
20	TAAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
25	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT	185

(2) INFORMATION FOR SEQ ID :281:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

30	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
35	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
40	TAAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
45	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA	186

(2) INFORMATION FOR SEQ ID :282:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

	TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTCGAGA GTCCATGTTC	50
	TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT	100
10	TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT	150
	GTAGGCACAG GGAGACTCAA AAGCACGAGT TNTGAAAGCG TAAATGGG	198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

	AGAAAAAAGGT GAAGCGAAC CCAAGGACAC CATGCTAAGG GCAAAAGTAA	50
	GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA	100
30	CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC	150
	CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTGG ACAGCTTCT	200
35	CAGCTCCCTG ACTCCGTTA CC	222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA	CTACCTCTAT	AATGAAGACT	GTTCTCAAAA	ACGCGAGGNA	50
ATGTGNGACG	ACACTGACCT	ATCAGACAAG	AGGGCATGCC	CCCCTGGCCA	100
10 CTTTGNCGC	TGTTTNTGCA	ACGTTCGCAG	TGNTACTCTG	CGTGAACCGG	150
TAGACTGCTT	GG				162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC	AAAGCCCACT	CCTCCAGGGT	GAAGTTTTC	TCCCGCGACA	50
30 GACAGCAGAC	TCGAGCC				67

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

	GGTCGGATCA GGTACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA	50
	GGCAGGGGCC CGGCCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT	100
5	TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA	150
	GAA	153

(2) INFORMATION FOR SEQ ID :287:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20	TACTACGGCT AAGGAGAAAC AATGTTCTA CATATCACGG GTAGTGAGAA	50
	CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT	100
25	CCATCGTGCT TTAGAAATAA CTGTATACAG TGTATATAAGT TGAAAAGAAC	150
	TCAAAATAAC TGATATAAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG	200
	CTTTCTGTGA AGTCAATCAG CTATATTAAC AATGACACAA ATCCAAAACC	250
30	GATGCATGCC ATATANAAGG GACATTGNA GTCCGCTCGC TGC	293

(2) INFORMATION FOR SEQ ID :288:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

	AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT	50
5	CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCC	100
	GTGTTGAATC ACTG	114

(2) INFORMATION FOR SEQ ID :289:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 290 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20	ATGAACCAGT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTGCTGGA	50
	AAGGACGTTG CCAGGACTTA CACGTTACA GATCCAGCAA CTGCTCTNCC	100
25	CAGTGCCACA ACCATGGGGC GCCAACCCACA AGCAGGAGTC CCACTGCCAC	150
	GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC	200
	AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT	250
30	GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT	290

(2) INFORMATION FOR SEQ ID :290:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 179 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

10 AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50
5 NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG 100
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTACTT TTGCTACTGT 150
TTTGTAGAAC GATGTACATG AATGAGCCT 179
10 (2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :291:
TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50
25 TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCGT AACTCTGCTT 100
CTGTGGGATT CTGCCAAGA GATCTCATTA CAGTTCCCAA TTCTTTGTTG 150
TTATAGTACC ATCACCATT CGTTAAATAG TGAAAGAGCT TTTTGAATC 199
30 (2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

	GGAAGACCAT TCTGATCATC CTCACTGACG CCP	GGCAA GAGGGTGGTT	50
	TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT		100
5	CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC		150
	AACCGAANNG ATATTACAAT GTAAAAA		177

(2) INFORMATION FOR SEQ ID :293:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

	ATTGGTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA	50
	CCAACCANAG CTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC	100
25	AAGGACAGCA GGNNGCTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT	150
	TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACTTGN GTCTGTTCT	200
	TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC	250
30	CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCCT	295

(2) INFORMATION FOR SEQ ID :294:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

	AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG	50
5	CATATTTAC CATTGGNAA ACTGTGAG	78

(2) INFORMATION FOR SEQ ID :295:

(i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 163 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

	ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT	50
20	GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG	100
	GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTTGAGA	150
25	GAGCCCGGTA ATA	163

(2) INFORMATION FOR SEQ ID :296:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 189 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

	AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC	50
40	CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA	100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCG GCGTNAGATG AAGAGGCCCT 150

CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCTTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid

- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCCTGTCCC CACTCACACA 50

AGTGGTCCGG TGTCACCCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100

20 GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150

GAAGAAGACA AGATGATCTG GTTACTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50

40 CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG 100

CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150

163

GTATCATCAT GCTGCCTCCT GCATTTGAAT T

181

(2) INFORMATION FOR SEQ ID :299:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15 AACATTGTTT ATTCATCCAG CAGTGGTGT CAGCTCCTAC CTCTGTGCCA 50
 GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTAGC ACAGCCTGGG 100
 GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA 150
 20 CTGCAAGCTG CTTGCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT 200
 CATCTGGTTG TGACTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT 250
 25 TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTCC 300
 GAGGCATGTA CATT 314

(2) INFORMATION FOR SEQ ID :300:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :300:

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC

50

164

	CACGCCAAC A GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT	100
	TTTAAGAACT GCCTAGAAAT CTCGTGTTAGG CACGAAGGGC TTGAGCCAGA	150
5	AAGGAGAGAC AAGTGCAA	168

(2) INFORMATION FOR SEQ ID :301:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :301:

	ACCCCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG	50
20	GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG	100
	CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT	142

25 (2) INFORMATION FOR SEQ ID :302:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

	AGAATTCTGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT	50
	GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG	100
40	AGGCCACAA GGACTCTCAT TGAGTTCTTA CTTCGTTCA GTCAAGACAA	150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

(2) INFORMATION FOR SEQ ID :303:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15	AGAATTGC ^{AA} CTCATC ^{CT} AA GTGGGCACAT TTAGACATAG CAGGCATGAT	50
	GACCAAC ^{AAA} GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC	100
	CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA	150
20	TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT	200
	AAAAGTTTTT GAATAATGA TGAAAATTTT TTAACT	236

25 (2) INFORMATION FOR SEQ ID :304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :304:

	ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC	50
	CATGTTCC ^{CT} TTAGTTCC ^{CA} GCACACGGGG CTCTGCAGTA GTGAATGAAG	100
40	TCTAGCACAG CCACCGCCCC CATGCCAGG CTCAGGAGCA CACTGAGGTC	150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200

TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50

20 ATGCCAAAGA AAGAAGGTCC TGGGGTTTT TATAGAAGCT CAAAAAGNTC 100

AACCTTCGAT GCTATCCCC AGCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

40 NGNTGATATA AACAGATNNA 120

(2) INFORMATION FOR SEQ ID :307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT	50
TNGCTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG	100
NGNTGATATA AACAGATNNA	120

(2) INFORMATION FOR SEQ ID :308:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :308:

30

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT	50
AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA	100
GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC	150
TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG	200
AGCCGGGGGT TATAACATCA AGTCTGTCT TGACCTCACA AAGCCAG	247

(2) INFORMATION FOR SEQ ID :309:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs

168

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

10	AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG	50
	AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACTGTGA TACGTATAAT	100
	ATGCGTT	107

15 (2) INFORMATION FOR SEQ ID :310:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 114 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

	GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG	50
30	ATTCTGGGGT CCACCCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG	100
	TATCAGGAAA GAGA	114

(2) INFORMATION FOR SEQ ID :311:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 237 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

	ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCCACCAT AACCCCAC	50
5	TCCACTGCCT CCTGGACCAT AGTTTCTCC ACTATACGGT CCCCCCATGT	100
	TCCCTGCTACC ACCAAAGTTT CCACCTTTA TCGAACCGTA TTAGAAGGTC	150
	GCTGGTTATA ATTTCCAAA TATGTAATT CCACCTCCAA ATCCTTTATA	200
10	GTTGTCATAA CCACCTCCGT AGCCCCCACC CTGTTGC	237

(2) INFORMATION FOR SEQ ID :312:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 147 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25	TNNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG	50
	TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA	100
	GAGAACTTGG CAATAGCAAG TACAGACAAAC TATGTGAGAA ATACTGC	147

30

(2) INFORMATION FOR SEQ ID :313:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 151 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

5 CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50
CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150
G 151

(2) INFORMATION FOR SEQ ID :314:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20 GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100
25 AAGGCTAATG GCACAACGTG CCACGTAGGC ATTCAACCCCA GCAAGGTGGT 150
TATCACTAGG CTAAAACCTGG ACAAAAGACCG CAAAAAGATC CTCGAACGGA 200
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA 287

(2) INFORMATION FOR SEQ ID :315:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

5 GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTCT 50
 GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTCCA 100
 CCTTGCAGC CTGTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150
 GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183
10

(2) INFORMATION FOR SEQ ID :316:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 20
 (xi) SEQUENCE DESCRIPTION: SEQ ID :316:

25 GGAATGAATC AACGNCTCT ATAATGAAGA TAATGTTCA GAAACGTGGG 50
 TTCTGTGCGT GCACTGATT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100
 CCACCTTGC AGCCTGTTTC TGTCAATGTAG TTTCA 135

30 (2) INFORMATION FOR SEQ ID :317:
 30
 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :317:
 CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

	TGCCGAAGTC CAAAAGCTTC AGCATTCTC TAGTGTCAAGG ATCTACTTCA	100
	ATAATNNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC	150
5	CTATNTTTTC TGCGGCTTGA TGGAGATACC TTTACTG	187

(2) INFORMATION FOR SEQ ID :318:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 268 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :318:

	TCCCAGGAGA AGGAACCTTG AAATTCAATCC CAACGTAGGC TGAGTGACCT	50
20	GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT	100
	CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA	150
25	ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT	200
	GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN	250
	AGCTTTCNGT TGNNNTAA	268

30

(2) INFORMATION FOR SEQ ID :319:

	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 138 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA 50
AGATGAACAG ATAAGCTGGA CCAATAATT ACAGATTCCA CAGAGGGTGA 100
5 GGACACCCAG ATGCCAGG ACTGTAGGAA ATCACAAT 138

(2) INFORMATION FOR SEQ ID :320:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :320:

20 AAAATGATGAT AAATTCACTCC TCTTCTGCTC TTAAAATTTC ATAAACCTCA 50
GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100
GTAATCATAC TTCCCCCA 118

25 (2) INFORMATION FOR SEQ ID :321:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50
GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100
40 GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

TTCCTTTCC

160

(2) INFORMATION FOR SEQ ID :322:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15	AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCG	50
	AACAGGGCTG CTGATTGTTTC CTTTCACTTT TGNGGTGACC TTGAGCTCCC	100
	TTAAAAAAAAAA AACTTGGAGA ATCACAAC TG GCAATGCACC GCAGTTCTCG	150
20	AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTCC ATATCAACTT	200
	GTGGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA	250
25	ACCCCCCTGGG AGTATAATNN TCTCCATANA A	281

(2) INFORMATION FOR SEQ ID :323:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :323:

40	GGAATTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC	50
	ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG	99

175

(2) INFORMATION FOR SEQ ID :324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :324:

5	GGAATTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANC	GC 50
15	ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA	100
	CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA	150
	TTGCCCGCGT TTTTAGG	167

20

(2) INFORMATION FOR SEQ ID :325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :325:

25	TGATCCAACT CTTCCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA	50
35	AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG	100
	ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCTCTT	150
	TCGGGTGCG	160

40

(2) INFORMATION FOR SEQ ID :326:

176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10	GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT	50
	GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG	100
15	AACATGAGAG AGCAGAGTGC TCTC	124

(2) INFORMATION FOR SEQ ID :327:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 253 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :327:

30	AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA	50
	GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT	100
	CGACAATGTA ACTCTGCAA TCGATGGAGT CCTTTACCTG CCATCATGGA	150
35	CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG	200
	CTAGCTCAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA	250
	AGT	253

40

(2) INFORMATION FOR SEQ ID :328:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :328:

10

GAACCTCTGG GCTCTCATCC TCTCCTATTG	ACAGTGAAGC CCATGGCAAA	50
TAGAAGAAGC TCAGTATCGG CTCCTCCCAC CATAACCGCC TTNAATCGC		100
15 CTCCTGGACC ATAGTTTCTT CCACCATAAG TCCCCCATG CTCCTGCTAC		150
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT		200

20

(2) INFORMATION FOR SEQ ID :329:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC	50	
TCTTTCTTTT NTCGAAAATN ATAAAACGTC GTATTCTACT TTATATTTAA		100
35 TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG	150	
AGCAACAAATA GTTCATATGT TCATGTTGC TACTATCACA ATNCAACATA		200
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTA		250
40 GGATTACCAA CTCACTGCTG CCATGACCGA	280	

178

(2) INFORMATION FOR SEQ ID :330:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAAC	TTTATGGGG	AGAAAGGTCA	GCAGCTTCTC	TTTCTTTNT	50	
15	CGAAAATNAT	AAAACGTGCGT	ATTCTACTTT	ATATTTAATG	TAAGGAAGAA	100
	AATATACAAG	CCCATATTAA	CATCGTATTT	CTATTAAGAG	CAACAATAGT	150
20	TCATATGTT	ATGTTGCTA	CTATCACAAT	NCAACATATG	AACACAGATC	200
	AGCTCTATAC	CATGAATACT	GCTGGAAGTG	ATGGTTTAGG	ATTACCAACT	250
	CACTGCTGCC	ATGACCGA				268

25

(2) INFORMATION FOR SEQ ID :331:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA	AGGAACCTAT	ACACCCTTA	TAGAGCTTTA	AATCGACTGT	50	
40	AGAGTTTGT	GGTCTTCCAG	TCCCAAATGT	TTAATTTCC	ATTTGCATTN	100
	TGAAATCACA	TAACTCATGT	CTGAAAAGTC	CACCTGACAA	GCATACCTGC	150

179

TACCATATGC CCTTAAAAAT

170

(2) INFORMATION FOR SEQ ID :332:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15 TCGCAGGAGA AGGAACCTAT ACACCCTTA TAGAGCTTTA AATCGACTGT 50
AGAGTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTCC ATTTGCATTN 100
TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150
20 TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGGTTCTGT 200
GTTCCAAAAA TNTAAGATT GTT 223

25 (2) INFORMATION FOR SEQ ID :333:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAACTCCCA CAAGTTCTTC 50
TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG 100
40 TCACAAAGGCT CATGTGCTTC ACCAAGGCAC TC 132

180

(2) INFORMATION FOR SEQ ID :334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA	TGGNAGGCAT	TTATCCTNTC	AATAATNC	ACGAGGCTTC	50	
15	TGGAATAACC	AGTGCCCCAT	TCCATCAGAG	TCTTGCGCG	ACTAAAGCCT	100
	CCATNTTG	CAATTCAAT	TGTTTGGGAT	TCTAGCACTC	CTTACCNGCA	150
20	GTAATGCC	TGCTGCAGAC	AACAACACCT	GGACTGNGAG	ATGGACCAAT	200
	TCTCAATGG	C AATCCAGGGA	AAGAGTGATC	CTTCT		235

(2) INFORMATION FOR SEQ ID :335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35	ATGCCCGCAC	CATCCGCTAC	CCCGATCCCC	TCATCAAGGT	GAATGATA	ACC 50	
	ATT	CAGATTG	ATT	TAGAGAC	TGGCAAGATT	ACTGATTCA	TCAAGTTCGA 100
	CACTGG	TAAC	CTGTGTATGG	TGACTGAGGT	GCTAACCTAG	GAAGAATTGG 150	
40	GNGATCACCA	ACAGGAGAG					169

181

(2) INFORMATION FOR SEQ ID :336:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCGCAC	CATCCGCTAC	CCCGATCCCC	TCATCAAGGT	GAATGATAACC	50	
15	ATTCAGATTG	ATTAGAGAC	TGGCAAGATT	ACTGATTCA	TCAAGTTCGA	100
	CACTGGTAAC	CTGTGTATGG	TGACTGAGGT	GCTAACCTAG	GAAGAATTGG	150
20	GNGATCACCA	ACAGGAGAGG	CACNCTGNAN	TCTTTGGCN	NNG	193

(2) INFORMATION FOR SEQ ID :337:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT	CCACAAGTTC	TTTGTCTAGG	ACTTCTAGCT	GCTCAGACCC	50	
35	TCAGGGTCTT	TGGATTGTTA	CCAAAGTCTG	TCAAACAGAC	CAGTAGTTA	100
	ATACCTGTAC	AGAAAAATGT	TTCTATTATG	CTTCTAGTAT	CTAGAAATTG	150
	CTTGCTACAG	CATGGAGGTG	GTTCTGCCCTT	TCCCTGGCTC	CTCACACTCT	200
40	CATCTGCAGG	ATTCCCAGCT	TTGCTCAGTC	TTCATGCCA	CCAGAGGCAA	250

182

AAAGGCAAAAC TAAAACGTGTC ATGCAGTGTT AGGTTGAAA TNAGCTGCTG 300

CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CACAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50

20 CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTAA 100

TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150

TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200

25 ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCAC CAGAGGCAAA 250

AAGGCAAACT AAAACTGTCA TGCAAGTGGTA GGTTTGAAAT NAGCTGCTGC 300

30 ATCAT 305

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

	AATATAAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA	50
	ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG	100
5	G	101

(2) INFORMATION FOR SEQ ID :340:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 113 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :340:

	GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGCGCA GGGGGCGTGG	50
20	AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA	100
	AGGACTTCCC GCA	113

25 (2) INFORMATION FOR SEQ ID :341:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 209 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :341:

	ACACAAATAA CTACATNTAC GCAATATAAT NTTAAAAAT CCAAAGCAAT	50
	ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTGGTG TATAACCGGC	100
40	AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA	150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200

TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

20 TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100

GCTTTTAATC TTCATTTTN NNNTTTGTNA TGGTAGGCTG AGATGCTTT 150

25 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTT 200

TACCCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250

TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :343:

40

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

	TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA	100
	GCTTTTAATC TTCATTTTN NNNTTTGTNA TGGTAGGCTG AGATGCTTT	150
5	AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTT	200
	TACCCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC	250
	TACAAAAC	258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 227 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

	GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC	50
25	CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG	100
	ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA	150
	TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG	200
30	CACAGGACCC AGGAGTCCGC CCACCTG	227

30

(2) INFORMATION FOR SEQ ID :345:

35 (i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 188 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

	AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG	50
5	TAAATGTTGA TTGAATACTA ACAAAAGTAGT GAAAGCAGAC GACACAGTAC	100
	CTGGCACACT ACTAAACTGT AAATGTTTC AAATCTGAAT CTGTAGAATT	150
	CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA	188
10		

(2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 262 base pairs
15	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :346:	
	AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG	50
25	TAAATGTTGA TTGAATACTA ACAAAAGTAGT GAAAGCAGAC GACACAGTAC	100
	CTGGCACACT ACTAAACTGT AAATGTTTC AAATCTGAAT CTGTAGAATT	150
	CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT	200
30	NNCTNNNAGG TTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC	250
	TAGAAGTGNA AA	262

(2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 159 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5	CTCTGTTTC CAAACGCCA TGTGTGCTAT ACTACAACTC TTCTCGAGTC	50
	TGATCAATT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC	100
	ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTTAAAAGA	150
10	AATNTCTAA	159

(2) INFORMATION FOR SEQ ID :348:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 283 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :348:

25	TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC	50
	ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT	100
	ACAATCGCAC CAATTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC	150
30	CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCCCTTCC CGGGACCCCTC	200
	TGGGAGCCGT TCGCNCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA	250
	TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC	283

35

(2) INFORMATION FOR SEQ ID :349:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 169 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5	CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGGA	50
	CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTAA AACATTCCC	100
	GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNAG GCTGAGCGGG	150
10	TGGATCACCC AGGTCAGGA	169

(2) INFORMATION FOR SEQ ID :350:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 175 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		

(xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25	GAAGNAACCA GTACCAAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC	50
	AACCCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT	100
	GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA	150
30	CTTGGCAACA NCACAGGAAG GGACC	175

(2) INFORMATION FOR SEQ ID :351:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 206 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

(xi) SEQUENCE DESCRIPTION: SEQ ID :351:

	AAATAAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA	50
5	AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG	100
	GCACACTACT AACTGTAAAT GTTTTAAAT TGAATCTGTA AAATTTGTAA	150
	GGTTTTATGA ATATAATATT ATTAACATT ATTGCTCTGA ATTTTTNNNN	200
10		
	NAGGCT	206

(2) INFORMATION FOR SEQ ID :352:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 76 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		

(xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25	AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG	50
	GACTTTAAAG CCGACAGTGA AATTAT	76

(2) INFORMATION FOR SEQ ID :353:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 245 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40	ACATTTGGCC CTCAGACTGT AATTCACATA CTACTNTGAC TGATACTAGA	50
----	--	----

190

	TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTG TGAGACAAAA	100
	ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG	150
5	GGCACTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC	200
	GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCCTGAG CACCA	245

(2) INFORMATION FOR SEQ ID :354:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC	50
AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG	100
25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT	150
CTTTGGGTTG AGACTTTCA GNGACAAC	179

(2) INFORMATION FOR SEQ ID :355:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC	50
--	----

191

TCCAGCATGT TGTCAACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100

AAGGTGCAGC CAATTTNTT GTAAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAAACCTTC CACTTATAAC TGTNTCAGCC TGACTATAAT 50

GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGG AAGACTAACCA 50

35 AGATTTGGAC ATTGGAATGT TTACTGTTAT TCTTTAAGAA ACAACTACAA 100

AAAGAAAATG TCAACAAATT TTTCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs

192

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

10	AAGGAACAAAG TGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG	50
	ATCAGCTTGT CAATTTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT	100
	TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAACTGCA TCATGTCCCT	150
15	GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG	200
	GGNACATGAG CAGCAGCTGN TCTTTAAC	228

(2) INFORMATION FOR SEQ ID :359:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30

	CAGGAGCAAG GAGGCCATT TGCTGAGCTC TCACAGCTGC TAGAGATGCT	50
	CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGT TTTTCTGCCA	100
35	CACTCACCCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAACACAA	150
	CCAAGAAAAT GAATAAAACA GCCAAACTCG ACCTTCTTAT GCAGAAAATT	200
	GGCATGAGGG GCAAGCCCAA GGTCAATTGAC CTCACAAGGA ATGAGGCC	248

40

(2) INFORMATION FOR SEQ ID :360:

193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC	TCCTTGT	TTT AATCGTCCTG	CTGCTGCTGC	50
CGTTCCGTGT CGCGTCGCC	CC ACATGACCCT	GAGGTCGCAA	TGATGAGTCC	100
15 TCTCTGGTCA GACACCGCTG	GAAATGAATA	CCAGGCCTGA	CCTCAAGCAA	150
CCATGAACTA GCTATTAAGA	AATAACANNGG	NAGGGCGGCA	GCCGGATCGT	200
GNNGGCGTTT NTCTGNGCCG	CCC GTCTCAA	TCTNTGTTCT	GCTTCCAGAT	250
20 GCC				253

(2) INFORMATION FOR SEQ ID :361:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAACACG GGCTCCATCC	TGGCCTCCTG	TNCACCTTCG	AACAGATGCG	50
GATTAGCAAG CAGGAGCACA	CGAATCAAGC	CCCTCCAGCC	ACCAAATT	100
40 CTAAACNGGC TNGGCNATGT	CGTAGTTNGT	TGTCAGTNGA	TCGGTAGAGA	150
TAAT				154

194

(2) INFORMATION FOR SEQ ID :362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACACG	GGCTCCATCC	TGGCCTCCTG	TNCACCTTCG	AACAGATGCG	50	
15	GATTAGCAAG	CAGGAGCACA	CGAATCAAGC	CCCTCCAGCC	ACCAAATTT	100
	CTAACACNGGC	TNGGCNATGT	CGTAGTTNGT	TGTCAGTNGA	TCGGTAGAGA	150
20	TAATCCTGNC	CACGCCCT				168

20

(2) INFORMATION FOR SEQ ID :363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA	AGGAAGCTTT	GNCACCACTC	TACCATCAAA	NNGGAATTGA	50	
35	ACATTCCCAT	TAAGGCAGTA	AAACAAAAGC	CAATAGCAAA	CATGNATTTC	100
	ATTCAACCAT	TGATAGATCT	CTGCCGTTAT	TCTTCAGTTT	CTCTTCTCGT	150
	CTCTCTATTT	NTTTCTCTGG	TTGTCGACCA	GCTGACTNTG	NCATCGTT	198

40

(2) INFORMATION FOR SEQ ID :364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10 TTATACAAGT CAAACTTGGG AGGTCATAGT AAGCATAACCT ATGCTGAGAG 50
AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAAGCAAC 100
15 TCGTACACTT TCAAGTTAA A 121

(2) INFORMATION FOR SEQ ID :365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 20 (D) TOPOLOGY: linear

25
(xi) SEQUENCE DESCRIPTION: SEQ ID :365:
GGTAAGTTGT ATTTGGGCCA GAATTTAAA GAGCACTATT TCGACATTAA 50
30 AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAAGAGTT TTCAATGCTT 100
TCTAAAAGTT TCCTCTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150
35 GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT 200
CTCCAAGGGA G 211

(2) INFORMATION FOR SEQ ID :366:

40
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs

196

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

10	CGGCTACAGC ATCACATCCA CTAATGCAC AGTTGTTGAA GTCACGCCCT	50
	GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC	100
	ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA	150
15	AAGTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG	200
	ATACAGTGGC CTTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT	250
	TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG	285

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID : 367:

	GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG	50
35	GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA	100
	ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGGAGGG AGTGGTAGT	149

(2) INFORMATION FOR SEQ ID :368:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT	CTCACAGCCA	TTGCAGTACA	TGAGCTCCAT	AGAGACAGCG	50	
10	CCGGGGCAAG	TGAGAGCCGG	ACGAGCACTG	GCGACTTGTG	CCTCGCTGAG	100
	GCAATACTAT	AATANGCAAG	GAACCTTTGA	GGCCGAG	137	

15 (2) INFORMATION FOR SEQ ID :369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA	GTTCAAAAGA	AAAGAGAAAG	TGTTATTTT	CTGTTAGTGA	50	
30	CATGTAGTCC	CTTTGTTCTA	GTAGGAAAAA	AGGTGCCTAG	AGGTAGTATA	100
	TAGAGTAAAT	ATTGTTCCCT	TGCCTACTCG	TGCTTCCAAT	GATTAAGGAA	150
	ATGTTAAACA	NNNGTNAAAG	TCTGTTTGT	CAATGCGGGA	GT	192

35 (2) INFORMATION FOR SEQ ID :370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :370:

	GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTGGCCACC AGCTCAGAGA	50
5	CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT	100
	GAAGACCCCTA ACANGCTTT ATGATGGGG TCATATCTAT GGTCACGNAT	150
10	ATAGTAGAAA CCAAAAGAAT GTAAGTATT GTNNATGATT TAAAAAT	197

(2) INFORMATION FOR SEQ ID :371:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 114 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :371:

	GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATT	50
25	ATACACTCCC GGAGCTGAAA AAACCGAACCA TAAGGGAGTG CACAAGAGCC	100
	GGGCTTGGAA GAGG	114

30 (2) INFORMATION FOR SEQ ID :372:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 127 base pairs
	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :372:

	CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCCTCCACA TTCCCTTCAG	50
--	---	----

199

CTCCTAGTTG TTCCACCTTG GCTAACAAATT TACCAATCTT TTTTTCTATG 100

AACACGTTCT GCCTTGCTG CTACTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTC 50

TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCTTA CTCAGTAGCA 100

20 GGC GGACACG GCCATGGGTC AAGACACCCCT GCTTCATGGG GAAACCTTGT 150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200

25 CGTTAGCAGC AACTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAAGT 250

TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

	NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT	100
	CCGTGGGAAT CACTGTCTGA GTCTTGTGTC TAGTATTGAC AGATATAGCT	150
5	TTGTTCTTGG AGTAGAATTAA AGGAATTGCG	180

(2) INFORMATION FOR SEQ ID :375:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :375:

	GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGCAA GAGGGTGGTT	50
20	TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC	100
	TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT	150
25	TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAAC ATCTTACTGA	200
	TGCTTACTTC AAGAAGAAGA AGCTGCCGAA GCCCAGACAC CAGGAACGTG	250
	AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA	300
30	TTGATCAGAA AGCTGTGGAC TTA	323

(2) INFORMATION FOR SEQ ID :376:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

201

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

	GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTT CTAAGAGGTG	50
5	AAATCACTCG CTGGTGTAA TTTCGGCACA ACCAGAAAAT AGTGNGGAT	100
	ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTCAGCTT ACATTCACAG	150
	ATGGGGGGTA GTTTTATAT TCTATAAGCG ACCATATTAA ANGCAATATG	200
10	AGTCAGTCCT GCATTTATGT CTT	223

(2) INFORMATION FOR SEQ ID :377:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 122 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25	GGCTCAGGAT CCGGCATCCT TTATGCCCTCC ACAGCACCTT GCTCTTCCC	50
	CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTGTCAT	100
	ATGGCTAATC AAGAGCCAGG TA	122

30

(2) INFORMATION FOR SEQ ID :378:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 195 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

	GGCAGTGCCT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC	50
	TACAAGGTGG ATAATACCTTC GGTACCTTGC TTGCCACAGC CCTGTTCCCTC	100
5	AAAGCTGAAT TGATAAAATT CTCTTGACT TCCAAGACCT AGCAGTTATA	150
	AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT	195

(2) INFORMATION FOR SEQ ID :379:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

	GTAGCCCTGA GGTCACTCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG	50
	GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACCTG GAAGGTTATA	100
25	GTAAGCATACTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN	150
	GGTTTNTNGN AACAAAGCAA CTTGTAATT AAGNTTAAAC NGAGCATCAT	200
	ATANNNNNGG	210

30

(2) INFORMATION FOR SEQ ID :380:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

203

	CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT	50
	GCAC TGTCAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA	100
5	ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTACCCCCA	150
	CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG	200
	GCCCACAAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA	238

10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

	GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA	50
25	ATAGCTGTTCAACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCAC	100
	CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTCAAAC	150
	GATTGGAAAT CTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA	200
30	AGCGTCAGCA AAGAGACCCCT CTCTGCACCA ATAAAACAGG TGGAAGAAAA	250
	CCTAGCNCGC ACAGAACATA AGCTC	275

35

(2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- 40 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCCCA ACACTTAAA 50
 CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA 96

(2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGACTTGATG GCTTCTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50
 AGGAGCTCTG GGCACCCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100
 TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTCAT 150
25 CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG 196

(2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCC A TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50
 ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA 100

205

	CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG	150
	CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT	200
5	CCCCAT	206

(2) INFORMATION FOR SEQ ID :385:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 134 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

	GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTCAC	50
20	CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG	100
	AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA	134

25 (2) INFORMATION FOR SEQ ID :386:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 161 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :386:

	CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC	50
40	ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA	100
	CCAGGACGCC ACGCCGACGA ACAAGGGAG TTCNGAGGAG GAGGAGGCCA	150

GGACGAGGCG T

161

(2) INFORMATION FOR SEQ ID :387:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESC ECTION: SEQ ID :387:

15	GGTGAGCCTC CGCCATCCAG C	CAAAC TGTGC AGAC CGCAGCTGTG	50
	CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGA	CAC TGAAAACACA	100
	ACCAGTCAAT GCCGTGTGGT TTTGTTGAA TATAATNGC	TGAAAGTGTG	150
20	GT	TTTTTTNAG GCAGTAATNT	170

(2) INFORMATION FOR SEQ ID :388:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35	TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA	GAAGGTCCTG	50
	GGGTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATG	CTATCCCCA	100
	GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAC	GGCTTCGGTT	150
40	TCTTTTTCT CTTAATNNC CTACAATNGC TTTACATATT	CGTGTGCAGC	200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTCA AACTGAAATC

250

(2) INFORMATION FOR SEQ ID :389:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15	GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT	50
	CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTNA GTACCCCTCCT	100
	CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN	150
20	TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG	200
	AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC	250
25	GTAGGGCNTG AGGGAGGT	268

(2) INFORMATION FOR SEQ ID :390:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

40	GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA	50
	GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT	100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG	150
CCAGGTATAAC ACCTTANAGA GGATGAC	177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA	50
TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG	100
20 GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAA	139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTGCC	50
TATCTGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC	100
40 AGCCACCCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA	150
AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACCGGGAG	200

209

AAGAAAATTG ACAAATAATA GAGGTCTCA AGCCCACGGA CTCCTGGTCT 250

GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTGGAAG GTACTGGTCC AATTATCTA GGAAGTATCT 50

20 CTTGGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG 100

CTGGCATTCT GGGGCTACC AAAACACCCC TCNNNGAGTA GAAGCTGCTG 150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50

40 AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA 97

(2) INFORMATION FOR SEQ ID :395:

210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10 AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTC 50
 GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100
 CCCTTGACTG ATTTATTGTC GTCAAAAGCA TGTTCCCTCTA TCTTTTNNNN 150
 TCAGACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT 200
 AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT 244
20

(2) INFORMATION FOR SEQ ID :396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50
35 TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100
 GCTTTGCAGT GAAGTATACT AGCAATAATT TTCGTACCTG ATCAAGTTA 150
 TTGCAGCCTT TCTTTCCGT TTCTTTNTG AAGGG 185
40

(2) INFORMATION FOR SEQ ID :397:

211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :397:

10

GGACACATCC	ACCCAGTGAA	CTGGACTGTG	GCCATGACCC	AGGGTATCAG	50	
CTCCAAACTC	TGCCAGGGCT	GAGAGACACA	TGAAGGAAGA	TGATGGGAGG	100	
15	AAAAGCCCAG	GAGAAGTCCA	CCAGGGACCA	GCCCAGCCTG	TATACTTGCC	150
	ACTTACCACC	AGGACTCCTT	GNTCTGCTCT	GGCAAGAGAC	TCTTGTCTGA	200
20	ACACTGCTTA	TCTGACCC				218

20

(2) INFORMATION FOR SEQ ID :398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :398:

GGAAGCAAAA	AAACAAAAC	AAGCTCGAAT	TTGCTTCAA	ACCTGTAGAT	50	
35	TGCATCTAAC	CANGTGTCCC	TATGCACCTC	AGAGTACTGG	AATACGAACC	100
	CAGCGAGACC	TTGTCCCCTC	CCATTTGCT	GNACTTTGT	TGGTGAAAAT	150
	GAGAATGAGT	TNATCCCTAC	NTACTTAGTT	TAATGCATTT	GACCCCAGAA	200
40	AACCCCAAGTA	CCTTNNACA	ATGACCCAAC	CANTACCTAC	CATCGGCCAG	250

(2) INFORMATION FOR SEQ ID :399:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :399:

	TCACTTGATT CATCCGTCGC GGGATTTGGG AGCACTAGCA ACATAATCAA	50
15	CACACTCCTA CAATCTTAGG CTTCACATGT GCTGATGATG ATGAAACCAA	100
	CTCTGCCCAA ATCATCTCCC CTTCTNTTAG GGTCTTACTA CATATCGCAA	150
20	CAGAAGATAA TATTGAGGTG AAGAGGGCTAA CATGAAGTTT GGCAC TACCC	200
	TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAAC T GATGTCCAA	250
	ATAATGAGAT TAAATTTATG TTTCGAGT	278

25

(2) INFORMATION FOR SEQ ID :400:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :400:

	GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA	50
	GCAGGGAAAGGA ATTAGAGCCT TCTGCTTTG CACCTGCTTT GAGTTAGGAA	100
40	GCAAGCTCTC TTCCCTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTA	150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA

200

ATGTGTT

207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA

50

GGGGGCCAGC CTGGGGCCTG GGCCTTTAA TCTAAGGACT GGGGAGAAC

100

20

AAGGGACCTT AGAGGTCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC

150

AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG

200

25

NTTCTCCAAA GATAGCC

217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTCACCTT CANTTAGTC AGAGTTGTTG ATTCAAGACT

50

40

CTTCCCCACAC TCGCACATCG AAACATTTT GTGCCAGGGC TTTCCAGCTC

100

214

	CAATTATCTT CTCGACAGCA TATACAGAAT CCCCCACATCT GGAACACTTC	150
	TCAGCACCTC CATANNTTGA GCAAATTAG AAGTGTGTTGG ATTTGTGTA	200
5	GGCCTGTGAG GCTGAACACT CTCTG	225

(2) INFORMATION FOR SEQ ID :403:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :403:

	AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG	50
20	ACTGNGGCTT CCACTGCGCC CGTGTACNTT ATCGAAGCTA CAGAT	95

(2) INFORMATION FOR SEQ ID :404:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :404:

35	AGGAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG	50
	CAAATTCCAA AACAGAAAAG ATTCAACAATN NAAAGGTGCA TACATTAAG	100
	GGCCACACTG TGTAATACTG TGCCAACTTA TGGAGTCTC ATTGTTCAAG	150
40	ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATAACC	200

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

(2) INFORMATION FOR SEQ ID :405:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15

GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA

50

TGTTCCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG

100

20

AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA

150

GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC

189

(2) INFORMATION FOR SEQ ID :406:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35

CACCATCCTC CAAGTAAATC CCCCCCTTAGG AAAGTAAGGG AAAAGACCCC

50

TTATAGCCCT GAGCTCCCC TTGGA

75

(2) INFORMATION FOR SEQ ID :407:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs

216

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

10	TATTCATCCA GCAGTGGTGC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT	50
15	TTTCATATCT AAGATCAATT CCCTCTTTA GCACAGCCTG GGGAGGGNGT	100
20	CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG	150
25	CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC	190

(2) INFORMATION FOR SEQ ID :408:

20	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 194 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

30	GAAGACATGG CGCCCTAACCA CTTCGAGACC TGCTGNTAAA TTAAAAGCTA	50
35	TTTTTCATTA AACCAACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG	100
40	CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG	150
45	CACTTTCATC ATGGACTAAG AATCCTTGCT GTGGNCNTGA TCTT	194

(2) INFORMATION FOR SEQ ID :409:

40	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGTH: 97 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAAG AGTCATCCAT GGATACAGTT CCAATCATTA TAACCACCTTC	50
TAAAAACAAGA TCATCTTCTG CAGCACCTGG TTTTAGTTTA TCCTTGA	97
10	

(2) INFORMATION FOR SEQ ID :410:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG	50
25 ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNNTNTG GTCCAGGGCC	100
AGCTCTTCCG AGGCTCCAGC CTGCTTTCG CCGGTGTCAT CAGATCATGC	150
TTTGC	155

30

(2) INFORMATION FOR SEQ ID :411:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

	AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCCGTA	50
	AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC	100
5	TCTGCTTCTG TGCTCCCTCC TGAGAACCT TTATGAGCCT GATTCCCTCAG	150
	TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA	200
	TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT	249

10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 143 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

	AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCA	50
25	TTTACTCCTC TATAACTCAT CTTCACACCN GCATATTTAA ACAAACTAAC	100
	AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT	143

30

(2) INFORMATION FOR SEQ ID :413:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCCCC ATTCACTGTAC TCCATCACAA AGTACAGGGCG GTCCATGGTC

50

219

	TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA	100
	CACCCACTTC TCCACCATAG TGCACCCAC GTCATCATCT GATCACAACG	150
5	TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT	200
	GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT	250
	AAAATC	256

10 (2) INFORMATION FOR SEQ ID :414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA	50
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC	87

(2) INFORMATION FOR SEQ ID :415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT	50
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCCGCCGC	100

220

	GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC	150
	ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG	200
5	CAGTGTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC	247

(2) INFORMATION FOR SEQ ID :416:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 162 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :416:

	TCTAGCACAC AGCTGCGCTC ACAAAAACGT CGCGACTTGT TAGAACTAAT	50
20	TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA	100
	TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATT	150
25	ACATTGAAAG GA	162

(2) INFORMATION FOR SEQ ID :417:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 109 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :417:

	CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA	50
40	GTACTTAGCA AAATATTTGT TTTNCGTGAT TTAGCTTGTC ATTAAACNAA	100

GAGCTACTG

109

(2) INFORMATION FOR SEQ ID :418:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15	GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT	50
	CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTT	100
	TAAATAGTAC ATATCATTAA ACCATTCTT CTAAANGTAA GAAGAGCAGA	150
20	AAAAATCTTA TAAGATTATC AGATTTCCCT AATGACACAG AAATGNAAGA	200
	AA	202

25 (2) INFORMATION FOR SEQ ID :419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

	TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC	50
	ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG	100
40	CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC	150

222

TA

152

(2) INFORMATION FOR SEQ ID :420:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15

CAGCCCTACA CTCGCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA

50

TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA

100

AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTGG

150

20

CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT

200

CTGCAATGTA GGGGCCGG

218

25

(2) INFORMATION FOR SEQ ID :421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAAACT CCCCCACCCA

50

GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC

100

40

CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGGCG CTTACTGTGC

150

223

TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC 200

ACTCCCTCAC CCCGGTGCCG GGCGTGCAG TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGNGTAATA AATACTGCAT CCTTTCCACA ACATAGCAGG AATCTTATAG 50

20 GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100

TTTCTTTACG AAGTGTAAAT AAGTGCTGCA CCATACTGTA AACAAAACTC 150

GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT 200

25 CC 202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50

40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAGTT CAACCTTTGA 100

224

	TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAAT	150
	ACTGACTTCG GTTTCTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA	200
5	TTCGTATCAG CACCTA	216

(2) INFORMATION FOR SEQ ID :424:

(i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 168 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :424:

20	CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT	50
	GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCCATA TGTCCCTCGC	100
	CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG	150
25	GGTGCCCTTT TAAAAAAA	168

(2) INFORMATION FOR SEQ ID :425:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 258 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :425:

40	TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC	50
	TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA	100

225

	GAGGAGTCAC AGTGGAACTT CCCAGCTTA AGATATCTAG CAGAAACTAT	150
	AGCTGAGGAC TAAGGAATTG TGCAGCTTGC AGATGTTAA GAAAATAATG	200
5	GCCAGATTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC	250
	TAATTAGG	258

(2) INFORMATION FOR SEQ ID :426:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 275 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20	TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG	50
	CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN	100
25	GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTGNN CAGCAAGCTC	150
	CATGCACGAA GGACTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG	200
	CTGAAACTCC AGGGTGGATA ATGCCCGTC AATTTGTGCC AGCTGCTGTT	250
30	CGAATNNNTT TCTTCTCGT AAAGC	275

(2) INFORMATION FOR SEQ ID :427:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 162 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

	CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA	50
5	GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTNTGGC AAACTGTCGG	100
	GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT	150
	CTAAGAGTGC TC	162

10

(2) INFORMATION FOR SEQ ID :428:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 220 base pairs
15	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :428:

	ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC	50
25	CCATAGTTCC TGAACTCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC	100
	TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTAAA	150
	GTCGNNTTA CAATGATTG NCCTGGACTG AAATTCAANGC TGCCTTAAGG	200
30	TGCTGATGAT ATTGAGAAGT	220

(2) INFORMATION FOR SEQ ID :429:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 185 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

	GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA	50
5	GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT	100
	GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG	150
10	GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA	185

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 277 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :430:
----	---

	GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC	50
25	TACCTGGTCG TGGGAGTAGT GGTCATCGTG GACCCAGGGG TGATCCCTAT	100
	CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC	150
30	TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG	200
	GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG	250
	GAAGACACCG CAGAGCTCAC TTACCAA	277

(2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 125 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGCCTGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGCGCTGGTC 50
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100
CAGCAAGGAG GAAGAAGTCA TTGTT 125

10 (2) INFORMATION FOR SEQ ID :432:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

25 GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50
TCGAAATAGC ACATTTTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100
GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150
AATTCCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200
30 ANAANGGAAA TGGGGCAGGA CA 222

(2) INFORMATION FOR SEQ ID :433:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

229

	CCATGNCGGC CCCCAGGTCC TCGATCTTT CGAGCTGACT TCTCATGGCT	50
	CGATTTCCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC	100
5	CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT	150
	TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT	200
	NGNCGTTTCC TCT	213

10

(2) INFORMATION FOR SEQ ID :434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

	CCATGNCGGC CCCCAGGTCC TCGATCTTT CGAGCTGACT TCTCATGGCT	50
25	CGATTTCCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC	100
	CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT	150
	TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT	200
30	NGNCGTTTCC TCTGCCGGTG T	221

30

(2) INFORMATION FOR SEQ ID :435:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

	ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT	50
5	TAGTATATTT TCGTTGTCAG	70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 163 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

20	AGTACGCAAT GCTTCCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT	50
	CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTGGA	100
	GACTGATTGA GTACAAAATG AAACTGTGCG TCAGCTTGAT CCATTTGTC	150
25	ACCCCTCAAGT AGG	163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 170 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

40	TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA	50
	AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA	100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150

CTCAGCAACC CCTGAATTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50

20 AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100

GGGTGGGAAT GGATCAAAGG TGTAAAACA GATCTGTCTC GTAACTGTGT 150

AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTCGAGA AACAAATAGTG TATGTGTTCC TATAGGTATG 50

40 AGTTATTCACTGCA ATCCTCTGCC GAAATGATNT 100

ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAAG CTTTCCAGTT GACACCAAGT 50

20 CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA 100

CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

40 GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

	ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT	150
	GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT	200
5	TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT	250
	GGTT	254

(2) INFORMATION FOR SEQ ID :442:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20	GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG	50
	CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG	100
25	CAAGGGGCCG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC	147

(2) INFORMATION FOR SEQ ID :443:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :443:

40	GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG	50
	CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG	100

234

CAAGGGGGCGG	ANGANGACCG	TTTNGNTTCC	TTGAAANGAG	CCCCAGCTNC	150
TCCGNGNGAG	ACGCAGTGG	CTNCGATGNT	TAGCNCTAGT	NNCCCGCT	198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT	AGGAGAACAA	TGTTCCCTACA	TATTATGGGT	AGTGAGACAT	50
TATCTGTATA	CAGGGACTGT	GATTATTTAA	AATATGCAGA	ACTTATTCA	100
20 TCTGTGCTTT	AGAAATAACT	GTATACAGTG	TTATAAGTGA	AAGAACTCAA	150
AATAACTAAT	ACCAAATATA	CACCTATGTA	TTAGAATTCA	AAAAGCTGCT	200
25 TTCTGTGA					208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTC	ACTACGGGNT	ATGTGCATTC	TGGGCTTAGT	AATGTCAAAT	50
40 CACTCTTCTC	TCCAGCTTGG	CCATTCCCTCA	TTCCCTTGCGG	GCCTGCCCTG	100

235

TAGACCACAG GCTAATGGAA TGTCCCCGTC TGNGTCATCA NATTCTGTAA 150

CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCGTGATT GGTGGATAAA 50

20 GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100

TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCTCA 150

AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200

25 CCACCCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCAC CTGTTTAGA 50

40 AATCTAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTTAGAC 100

236

	CATGACTGTT TGTTGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG	150
	CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GGTGCTCTGG	200
5	GGAGGAGAGA GGAGAGAACCA GGCTGTTTG GAAAATATCC AGCACTTG	250
	C	251

(2) INFORMATION FOR SEQ ID :448:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

	ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNNGCAGGA ACGTGATGGC	50
	AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT	100
25	ACAATNTAGT CTAGAAAAAT AAGTCAATTCTATAAAATAA GTTTTTAGAT	150
	CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA	200
	AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA	250
30	GTG	253

(2) INFORMATION FOR SEQ ID :449:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

	ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA	50
5	ATACCTCTGT AAGAACGAGA ATACACCATA TGTTATTCAC ATGTATAGGA	100
	GTGATAAGAA AAT	113

(2) INFORMATION FOR SEQ ID :450:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20	TAGCATCCAG GGGAAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA	50
	GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA	100
25	AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCCGAGAAG TCAAAGGTAG	150
	AAACTATTTG AGATCAAAGT CCTATAAAC AAGTTAAATG ATTCCAAGAG	200
	GTAAATAGGA G	211

(2) INFORMATION FOR SEQ ID :451:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 194 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

	CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG	50
	NATTCACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTNCTG	100
5	TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTTCAAGCA	150
	GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG	194

(2) INFORMATION FOR SEQ ID :452:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

	ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA	50
	TAGCATATTG AGAATATATT CTCTGGTCA AACCAAAGAT TTTGTGACAT	100
25	TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA	150
	CTATAGTGAT GCTTGCAA	168

(2) INFORMATION FOR SEQ ID :453:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

	CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCCAGAC GTGAACCAAT	50
--	--	----

239

	TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCCTTCAC	100
	TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACCTCCAGA	150
5	TCATCCTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA	200
	TAGGACGCCA GACTACACTG	220

(2) INFORMATION FOR SEQ ID :454:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 275 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20	GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA	50
	AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT	100
25	TGCTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT	150
	ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTCAA	200
	ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA	250
30	TAGTTTGCT TTGTCTTTAG CGGTT	275

(2) INFORMATION FOR SEQ ID :455:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 270 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

	TCGCAGAAGG AGGAACGGGG ACTTCCATC CCCTGAACCA AGGCATGTTA	50
5	ACACTTGGCT CCAGCATGTT GTCATCATTC AACAGAAAT CGCACAAATG	100
	CTACTGTGCC GGGGTGNAGC CAATTTCTT AAGTAAGTGC TGACTTCCTT	150
10	AACANNTATC TNTNTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTG	200
	TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA	250
	TGCTCTNGGG TCTGCCATT	270

(2) INFORMATION FOR SEQ ID :456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

	TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC	50
	ACGACCCCTG CGCTGGATAC GGCGACGGTT TCTCATTGCG CCTTTGCCAG	100
30	CTCTCATTG CTGAGGGGCA TAGACCTTT GATATCATCC AGGCTTTAGT	150
	TTCTTAAGGA GCAAAACAGC TTCCCTGNNC TTCTTGTAGC CTTCAACTTA	200
35	TTTAAACTAC CAAGGAAGTT CAGGAACCTTC CTCANACGA TGACCTTAG	250
	ACAT	254

(2) INFORMATION FOR SEQ ID :457:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs

241

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

	ACACTAACTG TTCCATCCGT TATATTTGCT GTGAGGAAAA TTAAGATTCC	50
10	TGTTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG	100
	TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACAC AACCAAGAGA	150
15	GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG	200
	TTTCCCCAAT GACTGTAATT TATAAACTAA AAATTG	236

(2) INFORMATION FOR SEQ ID :458:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 108 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30	GAGANNNNNTT NNGGNAAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG	50
	NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC	100
35	GCTGGTAT	108

(2) INFORMATION FOR SEQ ID :459:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 155 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

	ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC	50
	CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC	100
10	CCATGTTCCCT GCTACCACCA AAGTTCCAC TCTCCATTGG ACCGTAGTTA	150
	GAGGT	155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

	TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC	50
	CAACACGCAG TGGCAGTGTG TATTTCCCTT CTCTTTTTT GTAAATATT	100
30	CTGGTTTGTG GAGGTTACACA GACATGTGTT AGTATATCCT TGCCTGCATG	150
	TAGTTGTCA TTACTAGAC	169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :461:

	ACCNNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT	50
5	CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT	100
	TTTATCAGCG TACCTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG	150
10	GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT	184

(2) INFORMATION FOR SEQ ID :462:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 275 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :462:

	AGGAACCN TG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT	50
25	TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA	100
	GCATTTATC AGCGTACCTT TTTGCCATG CGCTACCTGC TATTGATGAA	150
30	GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGN	200
	AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTGGCCGT	250
	NNACTGNGTT GTTGGCGACA GATGT	275

35

(2) INFORMATION FOR SEQ ID :463:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 149 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5 AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA 50
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT 100
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA 149
10 (2) INFORMATION FOR SEQ ID :464:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :464:
ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATT 50

25 CATATCCAAG ATCAAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT 100
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG 150
CCCAAGTCAC ACAGCTAGTG AAGACCAGA 179

30 (2) INFORMATION FOR SEQ ID :465:
(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

	CTACCTCTGT GCCAGGGCAG CATTTCATA TCCAAGATCA ATTCCCTCTC	50
	TCAGCACAGC CTGGGAGGGG GTCATTGTTTC TCCTCGTCCA TCAGATCTCA	100
5	GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAAGA	150
	CCAGAG	156

(2) INFORMATION FOR SEQ ID :466:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

	ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAAACA AGGCAGGAGA	50
	CTGCTGGTTC TGGTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC	100
25	TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCA GGGCCTCACC	150
	ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG	186

(2) INFORMATION FOR SEQ ID :467:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

	TNNNGATGAN TATANAAGCA TCATNGACGG TATTTCCNG TCTTGNANTT	50
--	---	----

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

(2) INFORMATION FOR SEQ ID :468:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15	ACTAGAAAGTA CAGCATCCTG CTGAAAAAT GATTGTAATG GCTTCTCATA	50
	TGCAAGAGCA AGAACGCCGAG ATGACACAAA CTTTGCCTGG TATTTGTTGG	100
	AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTT	150
20	AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA	187

(2) INFORMATION FOR SEQ ID :469:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35	AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA	50
	GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT	100
	GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATCAA	150
40	ACATCGGCTT CGTTCTTT TCNCCTTGA ATNTTAATGT TTACATACTA	200

247

GTGTGCAGCA CCTACTTCTT NATGCCGTG AACTGAAATC TAGATTTAA

250

ACTGAA

256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT

50

GAAGTCTGAA TGGAGCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA

100

20 GAGGGTTTG

109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAAACTTT ATCAATCATA

50

GAGCCTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTGC TTGNAGACCT

100

ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTCT

139

40

(2) INFORMATION FOR SEQ ID :472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10	TCGCAGGAGA AGGAATGTTG CCAATAGGAA CGCCTGTAGA CTGTTCAGAA	50
	GAAATGCCCA AATGAGCCAG ATGAGAAAGGC TGAGGGCAGG GCTGCTTTG	100
15	GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGGA CTATTAACGG	150
	CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTACACGT	200
	GGCACTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA	250
20	TGGGAGACAT TT	262

(2) INFORMATION FOR SEQ ID :473:

25	(i) SEQUENCE CHARACTERISTICS:
	<ul style="list-style-type: none"> (A) LENGTH: 189 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35	ACAGAAGGAC TTTGTCTCTT TAGCTTGTAG AGCTCAATGA ACATTATCTC	50
	GGCAAATGAC TCTGCTTTCT CGAAGGTCTT TCTCCGCTCC AGGTTTACTT	100
	GCATCTCTCA TACCTNNNTAC AGCCAACATG AACACTCTAT GTATTTCTA	150
40	AGCTTTCNCTC TGTTCAAGAA CTTTGAATTT AAAACGTCT	189

(2) INFORMATION FOR SEQ ID :474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA	GC	AAACTTAA	ACTCGAACGC	ACGTAATAGT	GCTCATAATT	50
15	CTNTNAAGGA	CTTTAAACTT	TACTCNGTAT	GCTNTNTTGA	TGACTCTAGC	100
	AGCCTCGCTA	ACCTAGTTA	CCCCACTGTC	CCCACCGGCG	AACTNTTTGT	150
20	GTTAGTACGC	GNGTTA				166

20

(2) INFORMATION FOR SEQ ID :475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA	GTAACACTAA	AGAGCTGTAA	AGAACATTGA	AGGTGGTCAT	50	
35	TCCTTCAAAA	CTGTGTTTG	ACCACACAAG	GTGGGCATTA	ACAAACAAAT	100
	TCAACTTAA					109

40

(2) INFORMATION FOR SEQ ID :476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

10	TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA	50
	GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA	100
	CGGGTCACTC AGTTACGTTT AGCCACAGCC T	131

15 (2) INFORMATION FOR SEQ ID :477:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :477:

30	ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCTAC	50
	ATATATGGGT AGTGAGAACCA TTATCTGTAT AACAGGGAAC TGTGATTATT	100
	TAAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC	150
	AGTGTATATAA GTGAAAAGA ACTCAAAATA ACTAATACAA ATATACACTA	200
35	CGTATTAGAA TTCAAAAAAG CTGCTTCTG TGAAGTCAAT CAGCTATATT	250
	AAAAAAAGACA CAAAT	265

40 (2) INFORMATION FOR SEQ ID :478:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 182 base pairs

251

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :478:

AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAAGACC	50
10 TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTGTT	100
ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT	150
15 NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG	182

(2) INFORMATION FOR SEQ ID :479:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :479:

AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA	50
30 CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA	100
AACGGGAGCC TCTAAATCTT GGTCGGGACT GCTCGCCTGG AGCCGCACTC	150
35 TTGAGTCCGA GGCCATCTT	169

(2) INFORMATION FOR SEQ ID :480:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

	AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT	50
	CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTTCTGTC TCACCGGATA	100
10	TTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCCT	150
	GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA	200
15	ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC	238

(2) INFORMATION FOR SEQ ID :481:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

	TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC	50
30	TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCGAA GTCTGCAAGC	100
	AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG	150
35	ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCTGT CTGAGGGAGG	200

C

201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs

253

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

10	CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
10	CCGTTGATT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
	CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
15	ACNTTTTTAG AT	162

(2) INFORMATION FOR SEQ ID :483:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

30	ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
30	ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
	AGCGGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACTCNT NCCTGAACCT	150
35	GAGGGAAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
	CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAAACT	250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs

254

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

10	AACATTATCT TGACAAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG	50
	AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG	100
	ATTAGAATGT TAATGCCACT TTGATTAGAT CT	132

15 (2) INFORMATION FOR SEQ ID :485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :485:

	TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC	50
30	CGCATTCACT GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC	100
	ACGGACTTCT CGACACCATC AAGAGCGAC	129

(2) INFORMATION FOR SEQ ID :486:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

255

(xi) SEQUENCE DESCRIPTION: SEQ ID :486:

	TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG	50
5	AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG	100
	ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT	150
10	CATTGCACCTT CAACCATATC GA	172

(2) INFORMATION FOR SEQ ID :487:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 210 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :487:	
	ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA	50
25	TTTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA	100
	TATATACAAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAAACC	150
	AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC	200
30	TCAGATATAT	210

(2) INFORMATION FOR SEQ ID :488:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 90 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50
5 ANACGTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

20 ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAACATA CCGGGAGCCA 50
TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50
CCCCCTCTGG ACTCCATGCA CCAAGGTCAAT GGCCAGGAGC TCTTGGCAGC 100
40 TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150
GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCCCGA 186

257

(2) INFORMATION FOR SEQ ID :491:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :491:

	AGCCAAC TAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA	50
15	ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT	100
	TATAGCCCAT AAAAGGACCA AACAAAGTAAG CTGAATGACT GTGAAAATAT	150
20	GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG	200
	CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC	250
	TTCATATCGG AAA	263

25 (2) INFORMATION FOR SEQ ID :492:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :492:

	AGAGTGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT	50
	AAATNGGTGT GGGNGGTCCG CTTTTGGCCA TCATCGCACC CCCCCGGTCA	100
40	CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA	150

258

CCGTGGGTC

159

(2) INFORMATION FOR SEQ ID :493:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTC CACCAAGGTGA ACAGTCCTAC CTGCTTGGTA 50
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100
CAAATCAAGG TATCGGAAG AATAATTCC CCTCGATTCC ACAGGAGGGA 150
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

(2) INFORMATION FOR SEQ ID :494:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGCAG 150
40 GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGAGTG 188

259

(2) INFORMATION FOR SEQ ID :495:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC	CTTTATTGAC AATGAGAAGA	TGGAGTCCCG	50
15 GACGCATCTA TCCCTCTTG	GCCCTTACAG GTTGCACG	AGAGTGAGAC	100
GCCTTCCTGG ACCAGGGGAG	GGNGNGTTGG TNCTNTGN	GTGNGGGTNT	150
20 GTGGGNGCTG CTGGGGAGG			169

20

(2) INFORMATION FOR SEQ ID :496:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTTCTATGG	CTGCTGCTTC TAGGAGTCTC	TCGCTCATAG	50
35 AAAAGGCACA CACTGAAAGA	GGAAGCAGAT CCCATTGCTG	TGGAAGTCCC	100
ATTGTTAGGA AGCTCTGCTT	TTCTGGAGTT CAAATTCGCA	TTCATGATGC	150
40 TTTAAACCGT CAAGCTGGGT	GG		172

40

(2) INFORMATION FOR SEQ ID :497:

260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC	ACAAGAAAAC CTCCCTCCAG	50
TAAATNGGTG TGGGNNGTCC GCTTTGGCC ATCATCGCAC	CCCCCCCCGT	100
15 ACTGGGCCTT GTTGCCGGC ACTTGTNNN CNGGCTGGGT	GTGTACCGTA	150
ACCGTGGGTC CTCTGACAAG TGCCCTAACTC GGCCCACCCC	TTAGGGTGTG	200
TNTCATCGAA GTGTAGNGAA TGGTGGAACG TTTGTTGTN	GTGTGC	246

20

(2) INFORMATION FOR SEQ ID :498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :498:

GCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC	CCACGCAAGT	50
35 CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT	CCAAACACAG	100
CCACTATTT TGTTGTATAT CTTCATCTCA ATGGCGACAT	GGCCACTGCC	150
CAAGGAACCTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC	AGATGTCTGT	200
40 GAACATCGTG CGTTA		215

(2) INFORMATION FOR SEQ ID :499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :499:

	GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT	50
15	AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCCTGTTCC	100
	ACANGAAAAT AAAGCTAGGG AGGTGATTAA TCTATCCGAG AAAAAAGCCG	150
	GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT	195

20

(2) INFORMATION FOR SEQ ID :500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :500:

	GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT	50
35	GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA	100
	ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG	150
	TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG	200
40	CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGG	250

262

GTGGAGCTGT

260

(2) INFORMATION FOR SEQ ID :501:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15	AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAAATCT AATACTATAT	50
	TAAAATNCGTT GCTACAAAGT GTTTTGTTTC TCTAAAAAGT AGTTTTGCA	100
	TATCATTCTGA CCTCTTCACC CATNTGCTGG CTTATTTGCT TTATATACAA	150
20	CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA	200
	CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA	250
25	ACCATGGCTT GCCCAAAT	268

(2) INFORMATION FOR SEQ ID :502:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :502:

40	AAAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG	50
	GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACCG CTCTAGAGAC	100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA

150

CC

152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC

50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAAC

100

20

NTTCTAACAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T

141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCG

50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG

100

40 GCCGAGC

107

(2) INFORMATION FOR SEQ ID :505:

264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCCTCTTCT	GATAAATTTG	AGGGCCCGTT	TGTCCTTGG	GACCTTCAGT	50	
AACTCCATGG	CGCGCCATCG	TACGGGGCAA	ANACACACCT	CCCGAATCAT	100	
15	GTCCCGCACG	AACTTGGTGT	GTTCGGTCAG	ACGCCCGCGT	TNGGCNTGTG	150
	CTGGGCTTGC	TCACGTTCTT	GTCACTTGT	GGCCCTTGT	GAG	193

(2) INFORMATION FOR SEQ ID :506:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG	GCGTATGCAT	ACTACGCTAA	GGAGAAACAA	TGTCCTACA	50	
TATTACGGGT	AGTGAGAAC	TTATCTGTAT	AACAGGGAAC	TGTGATTATT	100	
35	TAAAAATAGC	AGAACTTATT	ANCTGTGCTT	TAGAAATAAC	TGTATACAGT	150
	GTTATAAGTT	GAAAAGAACT	CAAAATAACT	AATAAATATA	ACCTATGTAT	200
	TAGAATTAAA	AAAGCTGCTT	TCTGTGAAGT	CAATCAGCTA	TATTA	250
40	TGACACAAAT	CCAAACAAGA	TGCA			274

(2) INFORMATION FOR SEQ ID :507:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :507:

	CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA	50
15	AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA	100
	GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA	150
20	AGTGGTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA	200
	CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAAC AAGGAAGAAA	250
	CCATTGAGAA GATGCAGGAG TAAAGTATTA T	281

25

(2) INFORMATION FOR SEQ ID :508:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :508:

	AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG	50
40	CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA	100
	GCAGAGGGGA CAGAGATGAT GACCCTTCG CTCCCCCCTG CAAATGAGCC	150

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

(2) INFORMATION FOR SEQ ID :509:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15

AAATGCAAAA CTCACCGTGC ACACCTCTAG ATCCCTGCCA CAAAGAAATC

50

TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT

100

ATTT

104

20

(2) INFORMATION FOR SEQ ID :510:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

35

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGCAG

50

GGAAGCTAGA CCCAGAATCA GGAAAATCTG TTTCCTCGTC CCCAGACTCC

100

CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA

150

GACTTGCATC TGNATCTTGN A

171

40

(2) INFORMATION FOR SEQ ID :511:

267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10

ACTGTACCTA	TCATCCTGAA	AAACTTTATG	GGGGAGAAAG	GTCAGCAGCT	50	
TCTCTTCCTT	TTNATCGAAA	ATAATAAAAC	TGCGTATTCT	ACTTTAACTA	100	
15	AATGTAAGGA	AGAAAATATA	CAAGCCCATA	TTTAATGTAT	TTCTATNCGA	150
	GCAACAAATAG	TTCATATGTT	CATGTTTGCT	ACTATCACAA	TTCAACATAT	200
	GAACACAGAT	CAGCTCTATA	CCATGAATAC	TGCTGGAAGT	GATGGTTAG	250
20	GATTA					255

(2) INFORMATION FOR SEQ ID :512:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35

GAAAGATTGG	ACATGATTGC	GTTTATAAGA	ATGAGAGTGT	TAAATTGGAT	50	
TTCTTGCTTT	ATTTGTGACA	TTTCAGTTA	TTAGAAATCA	TGTTACCATT	100	
40	AGAAAAATTG	AAGTTTCCTA	GTAACAAAGT	AATTTGATTT	GTGTAACCTG	150
	ATAAAAGATT	TACTGACTTA	AGCTTTGTT	TTTTTCATA	AGCTGCTTT	200

GAGCTTTGTC

210

(2) INFORMATION FOR SEQ ID :513:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15	CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA	50
	AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG	100
	AACAGGGATT CTTTCCTTA CAAAGACCC AAAGATAACGT GGACAAAAAA	150
20	AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG	200
	AAGAAACAAA CGTGTGCATC CT	222

25 (2) INFORMATION FOR SEQ ID :514:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

	GCAGGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT	50
	GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTG TGACAGTGAC	100
40	AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA	150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAATA ATCTAANGTA 50

20 ACTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA 100

TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

40 CACTCACACACA CACATGCACT CACCTGCATA CACACACACT CATAACACAG 100

AACACTCATA CACACANGCT TGTGCACACA TGTTCATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTAAACA CGTGTGNACA NTGTACTCAG

200

ACACACACAG GTGTG

215

5 (2) INFORMATION FOR SEQ ID :517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACAGA

50

GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG

100

20 TGTGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC

150

AATCATGGGC CCTAGCCGNC CTNGTAATAC G

181

25 (2) INFORMATION FOR SEQ ID :518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT

50

GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT

100

40 AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA

150

271

	AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT	200
	CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA	250
5	CCTGGCAACT	260

(2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 115 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :519:

20	AAGCTAATAAC AATGGTCATT TCCAGACAAA TTTAAAGGAA ACACTAAGGC	50
	TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA	100
	CATGCTCTTT TTTTA	115

25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 175 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

	CANGTGGCTT CAATTAACCA ATNAGGAGCC TCNNAACATC CTGTCGCAGA	50
	AACTCCCAAT ATAAACGCC CCANACACTA ACACAAAACA GCCTTATTAA	100
40	CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT	150

GACTNATAGN TNGACCCACC TGTGA

175

(2) INFORMATION FOR SEQ ID :521:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15 ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT 50
 TCTGTGTGTG GCAC TGATTT ATCAAGACAA GAGGGACATG CTTCCCCCTG 100
 TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA 136

20

(2) INFORMATION FOR SEQ ID :522:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG 50
 35 GATATATTCTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT 100
 GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC 150
 TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC 200

40

(2) INFORMATION FOR SEQ ID :523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT	50
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA	100
15 CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC	150
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA	200
CATA	204

20

(2) INFORMATION FOR SEQ ID :524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT	50
35 GGCAACAAAGT GCAGGTTTTT TGGCTTCCT TGATTCATAT TGTGCAAGAC	100
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNNTCTAAN ATAATCCAAA	150
GAGGTCAATG TATCATCA	168

40

(2) INFORMATION FOR SEQ ID :525:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :525:

10	AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT	50
	AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA	100
15	GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC	150
	ATTTAATTAA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAAGTGT	200
	TTATCTCCCT CTGCATTCAAG ACCAGGCTCC TTAGTGCACT CATCAGACTA	250
20	TCGCTGCCCT TGCTGTCTGC TGTTGAGCCT TCACCACCAC T	291

(2) INFORMATION FOR SEQ ID :526:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30	(xi) SEQUENCE DESCRIPTION: SEQ ID :526:	
35	CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACTCA	50
	TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC	100
	CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGCG	150
40	AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT	200

GGGAAGC

207

(2) INFORMATION FOR SEQ ID :527:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15	AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTGAG TGAGATGGAC	50
	AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC	100
	CCAGCCAGAC TACATTCCT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC	150
20	CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC	200
	CTCTGACCCA GCTTCACC	218

25 (2) INFORMATION FOR SEQ ID :528:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

	AACCTNATGA CTCTCCATCC CCTTGAACCA AACATCTAGC ACTCAGCTCC	50
	AGCATATTTCA ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT	100
40	GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC	150

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200

TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAAGATGGA AGACTTGGCA 50

ACAAGTGCAG GTTTTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100

20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50

GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTT 100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150

40

TATGCACATG CTGGTGCTAC CCTCTCACT 179

(2) INFORMATION FOR SEQ ID :531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :531:

15	AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAAT ATCTTCTCAG	50
20	CATTCAAAAC AAAACGCATA AGTCATTCTT AACTTNAGAG CTTTATAGCA	100
25	TTTCCTAGA CAGGAAGGGA AAAAACAGTT AGCATTAAA AGTCCGGAAA	150
30	GCTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTG TCCAAATCCC	200
35	TTAT	204

(2) INFORMATION FOR SEQ ID :532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :532:

35	AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC	50
40	CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC	100
45	CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAAAATACC	150
50	CTTTCTTCAA AACTTAGCTC TGAATGGAGA AAC	183

(2) INFORMATION FOR SEQ ID :533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :533:

	GAAACAAAGTT CTCGCTCATC CCTGCATTTG TGCCAACCTTC AGCTTGCAAT	50
15	ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC	100
	TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG	150
20	TTTCACAAGC TGGTTGATGG TGCCCAC TAC CCGTGATCTG CTCGCTGGGG	200
	GACAGCCTCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT	250
	AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT	287

25

(2) INFORMATION FOR SEQ ID :534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :534:

	AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT	50
40	GACTTTTGCA GTCA GAGTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG	100
	GTGTCCCCCT GCTGCGTCTG TTTCAGCT GAGTTCTTGT GAATCTNTGT	150

TTAG

154

(2) INFORMATION FOR SEQ ID :535:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15	GATTACCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG	50
	GGCCTATTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA	100
	TAAAGCTACT GAAAACATATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG	150
20	GTATTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC	200
	CTAGGAAGGC AC	212

25 (2) INFORMATION FOR SEQ ID :536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

	GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATTTC	50
	ATCTGATTCC AGCCTGCTTG CAACCCCTGGA ATCCTCTTGT TCCCTGCTGC	100
40	CTGCCCTTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCCCT	150

280

NTCGGCAGTT GTCTTACT

168

(2) INFORMATION FOR SEQ ID :537:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15 CGGATCATT TTATCTGATT CCAGCCTGCT TGCAACCCCTG GAATCCTCTT 50
 GTTCCCTGCT GCCTGCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGAA 100
 GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNNTAA TGAAGTA 147

20

(2) INFORMATION FOR SEQ ID :538:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG 50
 GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT 100
 GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT 150
 GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA 200
 40 AATNAATGTA AACCCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC 250

(2) INFORMATION FOR SEQ ID :539:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :539:

	AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT	50
15	GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTTCGGGG ATGGTGAATG	100
	CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC	150
	CACTGGGATA GGGGTCTAAA AAAGTAAATT GGGC	184

20

(2) INFORMATION FOR SEQ ID :540:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :540:

	AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA	50
35	CCAGGGAAGT CACCCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTT	100
	CATCATCATG TCTCCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC	150
	AGAT	154

40

(2) INFORMATION FOR SEQ ID :541:

282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTCTTAAGAAGCTGTCAAATATG	GCAGTCTTTGATGTTAGTA	50
ATTTTGTGTTCTTCTGTGTTATTGGTTCAA	AGTACTGGCCTTTCCTTCA	100
TTTCCAGTAA TTATTTATA ACTATCACTT	TTAATTGAGT GGAAATTAGA	150
TGATTTGGTT ATACTGTGAA ACAGC		175

(2) INFORMATION FOR SEQ ID :542:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTTCCTGCAGCTGCCGTATGC	CTGAGTGACTAAGGGGCAGT	50
CGTGAGAGGCAGAGTCCAAGATCTCATTGG	TCGTTCCAGACTGCCGTCC	100
AGCCGTGCTGCTTCATCAGG	GCACACTCGCCGCCCTCCTGGGCCAGGTT	150
GCACATGTACAGGTACCCGT	CGGCGCACCCACCAACAAACGCGGTCTCTG	200
AATCGCGACTGGCNAACAGA	T	221

40

(2) INFORMATION FOR SEQ ID :543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG	50
GAGAAACATA CCTTGAGAGG GGGTTTCTT TAAAACTAGT GTTAGAAGCT	100
TAGGGATTTT TTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA	150
TTTGACTTGT GCCGACATTG CAAACTTTNT GACAGG	186

(2) INFORMATION FOR SEQ ID :544:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(i) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCTGCCT	50
TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA	100
CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT	150
GCC	153

(2) INFORMATION FOR SEQ ID :545:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

284

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

	GATTCA	GCTC	CAGC	ATC	CTT	GCCAC	CTCCC	CA	CCC	GGG	AG	TCAAG	GGT	CG	50
10	TTGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT													100	
	ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGAAAG													150	
15	CCCAGGCCTG T													161	

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 188 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

	AATAG	CCCTG	AGGT	CATC	CCT	GCAA	AGTGCG	TATC	AAAAAA	TACG	AA	GT	TA	50
30	GGGTGACAAA GTTGACAGT GATGTTATAC AAGTC													100
	AACT TGGAAGGTCA													150
	TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATC													188
35	TTGTTTA TTGTAACAAA GCAACTTGTA CACTTTA													188

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC	CATCCANTTA	GTTANCAGAA	ACTAATCAAA	AGAAAGTCTG	50	
ACAACTGCAC	TCCCCCTTGC	ATGCCATTCT	CTCAAGCCCA	TAATCTTGG	100	
10	GTATCCACAA	CGTGCAGAAGG	CCTACCCTTT	GTGTGTACTC	ATCTCACGTT	150
	TACGTATTTT	GTNGTTGAGG	AGCTCCTCTA	CAAATGTTGC	GTATCTTCCG	200
15	AATCACTCAT	TTAGAAAA				218

(2) INFORMATION FOR SEQ ID :548:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGGAGACC	ATCAGNCCCG	TGAAGACCAC	TCCTGACGTC	TCGTGT	46
30					

(2) INFORMATION FOR SEQ ID :549:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

	AGGGGGCTAA NGGTTGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG	50
	TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG	100
5	AGGGGCAAGA CACGACCTT AGTTTCCCCC TTGCGATAAN CTTCNC	146

(2) INFORMATION FOR SEQ ID :550:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :550:

20	AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA	50
	ATCCAATTAT ACTCTTCAG TTATTTAAC ATGTACAATT AAATTATTAT	100
	TGACTCTAGT CACCTTGTG TGCGAGCAAG TACTAGGTCT TATTCAATTCT	150
25	TTCTAACTAT TCCAGGCCCT TTTAATCAA GAAGGCTCCC TAGACCAAAA	200
	TTTTAAAAAG ACAATGCTAG G	221

(2) INFORMATION FOR SEQ ID :551:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :551:

	AAACATCGTT TATTCACTCA GCAGTGTTGC TCAGCTCCTA CCTCTGTGCC	50
--	--	----

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100

GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50

20 CAGTATCGCT CCTCCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100

TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTCACT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50

GAGGCGCTAA TCAATAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100

40 GAATAAAATTA CCTGTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150

NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

(2) INFORMATION FOR SEQ ID :554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :554:

5	ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT	50
15	GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG	100
	GAATAAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG	150
	NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC	198

20

(2) INFORMATION FOR SEQ ID :555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :555:

25	CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAAC TGAAGAACCTT	50
35	GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG	97

(2) INFORMATION FOR SEQ ID :556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

	TCTGCTGTCT GTCCGAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT	50
	GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA	100
10	GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG	150
	CTGTTCAGGT CTTCCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT	200
15	CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT	250
	CTTCAAGGGT GATCTTGTT	269

(2) INFORMATION FOR SEQ ID :557:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 245 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

	ACTCCCTCAA GGTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG	50
	ACCCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCC	100
35	GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAC	150
	AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG	200
	ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC	245

40	(2) INFORMATION FOR SEQ ID :558:
----	----------------------------------

290

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10 GAATTTAAAA AAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC 50
ACAAACCTTCG TTCCGCAGTT CATTAATCCG ACTCTGATGC TAAGGTGACA 100
15 GTGTATGTAA GTAGATTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT 150
GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT 183

(2) INFORMATION FOR SEQ ID :559:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30 GTCATCTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG 50
AGATGATTAC GTGATAATGA CTTTGGCGC TTAACCTTG ATCCCGGGTA 100
35 TGCTNAAGAA GCTGAC 116

(2) INFORMATION FOR SEQ ID :560:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

	CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC	50
	TGGATACGGC GACGGTTCT CATTGCCTT TGTCAAGCTCT CATTGCTGA	100
10	GAGGCATAGA CCTTTTGAT ATCATCAGGC TTTCCGTTT TAGGAGCAAA	150
	ACAGCTTCTT	160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

	GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC	50
	AAATGCACCC CGTTCCCTG TGCGAGATCG TTTGAATNAG ACCAGAAACT	100
30	G	101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTGAT 50
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100
TATGAGGAGT GGAATTTAG ATGTCTATTA CATTNGTCTT TTAAAAGAAA 150
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183
10

(2) INFORMATION FOR SEQ ID :563:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :563:
AGAGACACGT GAAATTCTATA TCTCAAANN C ACAGAGCTGA GACTTTGGC 50

25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTGGTA 100
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187
30

(2) INFORMATION FOR SEQ ID :564:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :564:

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50
 CACAGAAAAA TGGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100
5 GAGACACGAT CTAGGAAGCC TACCACTTG GCTGCTCACT GTATGCACAC 150
 AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200
 AANGTGACTA TTC 213
10

(2) INFORMATION FOR SEQ ID :565:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xii) SEQUENCE DESCRIPTION: SEQ ID :565:
 TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCCTG 50
 GGGTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100
25 CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT 150
 TTCTTTTTTT CCTTTAA 167

30 (2) INFORMATION FOR SEQ ID :566:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs

35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xii) SEQUENCE DESCRIPTION: SEQ ID :566:

294

	GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT	50
	GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT	100
5	TTGTCGATGA ATTGAGCAAC TGAGAACG	128

(2) INFORMATION FOR SEQ ID :567:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :567:

20	GGAGGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTTGGA	50
	AAGTAGTCCT CAATCTTCGA TTTCCCAGCA AGGACTTTCT CAGCNAGCGA	100
	TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT	150
25	GTTCAGATGT CTTGAACAGG TTAGAGCCTC CTGTAGGCAG TTGGNNTGGG	200
	NG	202

30

(2) INFORMATION FOR SEQ ID :568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :568:

40	ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA	50
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295

	AAACAAATAT AGTATAAAC A TTAAACAAAT GAACAATAAT CATCAATAGA	100
	CGGGTTACTT TCAAGGAAGA GTTGTGTTGT GACAAATTCT ACTCTTGATC	150
5	TA	152

(2) INFORMATION FOR SEQ ID :569:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

	CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC	50
20	CGCACCCCTG AATTCTCCG CAAATTCCT GCCGGCAAGG TCCCAGCATT	100
	TGAGGGGATG ATGGATTCTG TGTGTTGAG AGCAACGCCA TTGCCTATTA	150
25	CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T	181

(2) INFORMATION FOR SEQ ID :570:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 157 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

	ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT	50
40	AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCTCNNT	100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA

150

ATGCTTT

157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA

50

AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTGACC

100

20

AGGGTATGAT CTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTACAC

150

ACAGGTGGTC GTTCCTGTT GGACACTGTT TTATTTGTTT GAC

193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA

50

GAAGGATTG AGGAGGTTGG TGGAATTGT TGAAGGAGAG GGCGAGGAAG

100

40

AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG

150

CTTCCCTGTT TTAAACATGA AAGTGTGGC

179

(2) INFORMATION FOR SEQ ID :573:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15	AGGACCTCTA AGACATCCTT ATGACGACAG TTTGTCCAA GGGGATATCC	50
	ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTTAAAAAGA	100
	TTTTATTTCT GATCTTTGG CGATCTTCTT CTTGCCCATG NNGCTGTTAC	150
20	TTNGCNCGGG NAGCGGTTAA TTCTANCCGC TAGGTGTGC	189

(2) INFORMATION FOR SEQ ID :574:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35	GTGCCTCTA GGTTTGAAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG	50
	TAAAGGTGTT CATAGTTGA CTGTTCTAT GATTTTTTT CAAAGAATCG	100
	TCCTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTAA	150
40	ATGTATATCT TTTACGTCTC TACTCAGACC ATATTTNAAA GGGGCGCCTC	200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTG 250

GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50

CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATTTCAA CTCCGATCTT 50

35 CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150

CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTTGT	CAAGGTCAGG	50
GAACAGCACC CACAGAGGGC CTCTGGTCC CTCTCTGCTC	AACTCCCTCT	100
15 CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC	AGAAGGACTG	150
AGTCTTCCTC CTGGACTTCT GGTCCTGGTA GGCTGTGCTT	CATGCTCTCC	200
20 TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA	AAGAATATGA	250
CTTTG		255

(2) INFORMATION FOR SEQ ID :578:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGGAAAAG AACTGAAGA	AAAAAGACAG	50
CCTGTGGAAG AAGCTCAAAG GTTCTTGAA GAAGAAGAGA	AAAAATATGA	100
40 CATGATATCT TTGCTTTGA GTTCCTCACG CTCTCTGAAT	TTATTAGTTG	150
GACAATTCCA TATGCACCAT TCTGCTTCAA TATANCTCTT	NNGGTCTCTC	200

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC

250

TCTTGAGATA GTTTGTTTT

270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA

50

GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC

100

20

TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG

139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA

50

TGTTCGATCC AATTATTTTC TTGGATAAGT TTTCTTTCC TATNCCTNTN

100

40 GTTTGATAA TATAATAAG AAGATGAGGG GCCCA TATAGAGCTC

150

CTGAGNGACT TTTNGGAG

168

301

(2) INFORMATION FOR SEQ ID :581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC	TGTTTGGGAA	AAATAGGATT	TTAAAAATAT	GGTCATTAA	50	
15	TTTAGGTTTT	CTAACATCTA	CTTGGGGATG	TAGCCTCCAG	TGAGGTCAGT	100
	TAAGTGGGAC	AGAACCGGCA	GAGGAAAGAG	GTCTTGCTT	CCCCTGGGCC	150
20	CATTCTCCCT	GGCTGCCAGC	CCTTGAAGTC	AGAACACCAT	GGGAAAATTC	200
	AGGAGTCGGC	ACTGTAGCCG	TCAAGTGGCG	CTACTTTCCA	CA	242

(2) INFORMATION FOR SEQ ID :582:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :582:

35	GCATTTTCT	TGTGTGCTGT	TTATAATAGC	AAAGCAG	37
----	-----------	------------	------------	---------	----

(2) INFORMATION FOR SEQ ID :583:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

10	GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG	50
15	ACAAGAAACA CTTACCAACA AAAATATTTC AACAAACCCCA AAATAACTTA	100
20	CTCACAAATA TGCAAAATTA TCTATGGCAT AGTATTCGC ACTCGATGAC	150
25	ATTTAGAGAT AAAAAATCAA ATGGAGCTT	179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

30	AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC	50
35	AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA	100
40	GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT	150
45	TTGCGACCCAC AATNCACCCCT TCATTTCGTA ACTGCT	186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :585:

	ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAACTA AACTACAAAC	50
5	GCACTCACAT CGCTATAATC CTTTTAAGGA CTTAAACTTT ACTCCATTAA	100
	GACTTTATG ACTTCTAACCA ACCTCGCCAA CCTCCTCACC CCCCAC TATA	150
10	CCTCGGAGAA CTTTCGCGTA ATAACCACGT	180

(2) INFORMATION FOR SEQ ID :586:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 183 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :586:

	ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTG GCTAANNNNN	50
25	NTNCTNNNTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC	100
	TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG	150
30	AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG	183

(2) INFORMATION FOR SEQ ID :587:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 280 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

	AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTGN	50
	ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTAAGC GCACNTTAAA	100
5	GAAGGACATC AGNGAGAACCA AGAGAGCTGT AAGACGCCTC CNTACTGCTT	150
	GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG	200
	NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT	250
10	GAGACTGATG TGACNTTCCT GGGACTGNCA	280

(2) INFORMATION FOR SEQ ID :588:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 371 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25	GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA	50
	CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC	100
	TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC	150
30	AATGCCCTTG TGCCTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT	200
	TNTTTTGTG CTTTTGGGG TATTTTCATT AGTATTCAG CAAATCTCAT	250
35	GATAAAGGNC AAGGNCAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG	300
	ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT	350
	GNGNNGCANG CTTANCTATG A	371

40

(2) INFORMATION FOR SEQ ID :589:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10 GAGAGAGAAC ACTCCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA 50
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100
15 GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150
TGCTGNTCAT TCTTNCACGG NCCCCTTTA TAAT 184

(2) INFORMATION FOR SEQ ID :590:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30 GGGGGCCCGC CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCC 50
NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTCATG GATANGGTGN 100
35 GTAAAACCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCTTN 150
AANGGTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

40 (2) INFORMATION FOR SEQ ID :591:

306

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10 ATTCGCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC 50
NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCNGN 100
15 NAAAAAAACC CCCTGGGNNC GCTTTCAACC CCCAAACTTT CAAATTCCGC 150
CCCTTTNGGC NANGCCAAC CANNCCCCC CCCTTTTNC CGNCCCANNC 200
TTNGGNCTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247
20

(2) INFORMATION FOR SEQ ID :592:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :592:

GGAGGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTG 50
35 ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100
CCANGGATTA CGTGCAATG TCTTCAAAAA TAGANAATTTC ATTTTATATT 150
TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGGAA TGTGACAAAA 200
40 TACTATGATG ATTACAACTC ATTAAAGCAT AAATNTGCAT GATTTAACTN 250

307

	CATGTTCCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA	300
	TTTANGGCNT NNGTGCTTTG TAATGATTG NCNTTAGGTG AAGGGNTACT	350
5	TTTNTNNNTNC TTCNTAGTAG ATTNGNTNN NTCTTTTAA GAGGANTCNA	400
	NTTTCATGNG TAANCATCAT CTTTT	425

(2) INFORMATION FOR SEQ ID :593:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

	CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC	50
	GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAA	100
25	CGCGTGTGAA CACATGCGCG CNNCGCGCNC GCGATNCAAA GCTGAAATGT	150
	GCNNNGNCNGT CGTGNCGNA AATGTGAAAT GAACAAACAA CAATGAATGA	200
	ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA	250
30	ANCAAAAG	258

(2) INFORMATION FOR SEQ ID :594:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

	GACCCTAACAA	ATATGTACAA	AAATATAAAA	TGTAAATAAA	AAATACAAAC	50
5	AAATTTCCCTT	TTTAAAGTAC	TTTTAAGAAA	AAAAGCAGGG	CCTTGGAAAGT	100
	TTTGGTTCTT	TTTCCTCCC	CTGTTGCAAA	TTCTCATGGT	TTGGGTTGGG	150
	TGCTGGAGAG	CGCGTGTCA	CTGCGGGTGC	CTGCCACGT	GGGCGGGC	200
10	CTCTCTACTC	GAAGG				215

(2) INFORMATION FOR SEQ ID :595:

15	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 272 base pairs				
	(B) TYPE: nucleic acid				
	(C) STRANDEDNESS: double				
	(D) TOPOLOGY: linear				
20					

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25	GGGGCTGGTT	TGGTCATCCG	AGATCATTAA	AAATGGCTGA	CCCTAACAAAT	50
	ATGTACAAAA	ATATAAAATG	TAAATAAAAA	ATACAAACAA	ATTCCTTTT	100
	TAAAGTACTT	TTAAGAAAAA	AAGCAGGGCC	TTGGAAGTTT	TGGTTCTTT	150
30	TTCCTCCCT	GTTGCAAATT	CTCATGGTTT	GGGTTGGGTG	GTGGAGAGCG	200
	CGTGTCACTC	GCGGGTGGCA	CTGCCACGGT	GGGCAGGC	GCTCTCTACT	250
35	CGAAGGTGAC	CACGTTAGA	TT			272

(2) INFORMATION FOR SEQ ID :596:

	(i) SEQUENCE CHARACTERISTICS:				
40	(A) LENGTH: 250 base pairs				
	(B) TYPE: nucleic acid				
	(C) STRANDEDNESS: double				

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

	GACAAACTGT TGACACCCGG AGGCCTAAC GAGGATTCA GCTTCCATTA	50
	TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG	100
10	AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT	150
	CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCGAA CAGTAGAGGC	200
15	CTTCCTCAAA GAGGCTGCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG	250

(2) INFORMATION FOR SEQ ID :597:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

	CTGCCAAATA CTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA	50
30	AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT	100
	ATCAAGAAAC CAGACTGTGA TGACTGGGAG AGCGGGCTGA ATGCAATGAG	150
35	TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGAACTGCAC	200
	AAACTGGCCA CTGACAAAAA TGACC	225

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

310

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

10	ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTTAGAT TTTCATTAC	50
15	AAAAAAAGTC ATTACACATTT TACACTATAC ACGTTATGAT ATAATACAGG	100
20	AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA	150
25	CCTGTTGTTG TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGC	200
30	CACCAAGGGAC	210

(2) INFORMATION FOR SEQ ID :599:

20	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 116 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

30	AAAGGAGTTG ACTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC	50
35	AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT	100
	AGAAAGTAAAAA AAAAAAA	116

(2) INFORMATION FOR SEQ ID :600:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 107 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

	ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC	50
	CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA	100
10	TGGCCTC	107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

25	ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTAGC CAATGTTACC	50
	GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT	100
	TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC	150
30	ATTTTCTTTC CTTAGTGTAC CAA	173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

312

(xi) SEQUENCE DESCRIPTION: SEQ ID :602:

	GGAAGAGAAC ACATACACGA GGACCAAGTAC CTGATGAGGA CAAGAGAGAT	50
5	GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT	100
	CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA	150
10	GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC	200
	AAGTACCCAG TAGGAG	216

(2) INFORMATION FOR SEQ ID :603:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 213 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25	GAAAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAAA TCACATATGT	50
	TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA	100
	TTTCTAGGGC CCTTCTTGGG GAAAGGTTCA TATAATTTAG CATAACATACA	150
30	TATTCAGTGA ATGCATTCA ATATTACTAT ATAAACACTC TCAGCTACAA	200
	TGGTAATATA ATG	213

35 (2) INFORMATION FOR SEQ ID :604:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 219 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTCC 50
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGACTGGACC TCTGGTCTCA 100
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200
CTTCAAGAAG AAGAGCTGC 219

(2) INFORMATION FOR SEQ ID :605:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25 AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100
30 NNGA 104

(2) INFORMATION FOR SEQ ID :606:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

	AATAAAGCAT TCTCACAAACC TTTGTTGGGT CAATGATTCC TTTTTACCAC	50
	ANNTACAGAA TCTCCACCAT AGCATCATAA CCAACTCTGA GGAACTTCGC	100
5	ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA	150
	TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA	189

(2) INFORMATION FOR SEQ ID :607:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 171 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20	GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA	50
	GAGCTCGTAT TTATCCTTG CTTTNATNTG AGACCAAGCT AGCCCTGAGT	100
25	AATTTTANNT GGTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT	150
	GCCTTACGCA CATTCCTTTN T	171

(2) INFORMATION FOR SEQ ID :608:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 184 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40	GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA	50
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315

	TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAACTGTG	100
	ATTATTTAAA AACCGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA	150
5	TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA	184

(2) INFORMATION FOR SEQ ID :609:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 191 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

	GGGGACAGCT NNNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC	50
20	CTGTGATTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN	100
	TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC	150
25	TCTGTTACAC TAGGTGTTAGA GTTCCAGAAT GTTCTTTGT T	191

(2) INFORMATION FOR SEQ ID :610:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 172 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

	GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT	50
40	GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT	100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT

150

AGGTATGATT TTATAGGNAT AA

172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT

50

T

51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTCA AAAAAATAAA ACAGTATCTC

50

35

TTAACACTG

60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTCGGC CGCCA 25

25

(2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTACT ATGTTCGCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

318

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10 TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG 50
GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA 100
15 CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG 137

(2) INFORMATION FOR SEQ ID :617:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :617:

30 GCAGGGCAGT CTTGGTGTGC AGCCCCCTCTC CTCTCTGTCC CCTGACACTC 50
CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT 100
139 CAGAAATAAA GGGCCCATTG GAGGGATGAC CGCATTAC

35 (2) INFORMATION FOR SEQ ID :618:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5	TCTTCTTACT ACACTGGAAG TCTGAACCTGG GTGCCTGTTA CCGTCGAGGG	50
	TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG	100
	CCTNCNCTGA GNNCNGCCAG GCCATTGTTG ACACCCNNCAC CTCTCNCNTG	150
10	ANNNNCCCAA CCAGCCCCAT TNCCAACA	178

(2) INFORMATION FOR SEQ ID :619:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 73 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :619:

25	ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC	50
	TTCTGCGGCC GCCACCGCGT GGA	73

(2) INFORMATION FOR SEQ ID :620:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40	TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA	50
	AACTTTGGTA GAGGGTTCCGG TACGACTTAC GACACCTGGC CCTACGTCA	100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15

TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT

50

GGAAATGAGC TAAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNCC

100

CACTTCCTCC CATGCCCTCC AAA

123

20

(2) INFORMATION FOR SEQ ID :622:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

35

CACCCAAGAC CATCCTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA

50

AAAACATTTC NNGAGGAATT TTCAATTCC AGCTTAAAGA ACNNNCCAC

100

CAACATAACC AATTATGAA ANNNATTCA TTAAAAGGTA TAGAACCTCT

150

TGTNNNCATG ATGGCAAGGG ACA

173

40

(2) INFORMATION FOR SEQ ID :623:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10 TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGC 50
GGTGAAGGCA GCTGCTTCT CCTTCACCTTC TTTGGGTTAC TAGAGCAACT 100
15 TGTCAGTAGA TT 112

(2) INFORMATION FOR SEQ ID :624:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :624:

30 ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGC 50
GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100
AGGTCTGCAT CCCCTCCCC 119

35 (2) INFORMATION FOR SEQ ID :625:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAAAATCT GAAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGCGA GTGCGGCCTC TAGACAAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :628:

10

AAAAGAAGTA GGTGGTGTG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG 50

GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTAAAGTGA 100

15

CCGGCAGC 108

(2) INFORMATION FOR SEQ ID :629:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :629:

30

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50

CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

(2) INFORMATION FOR SEQ ID :630:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

	CCAGCNCCGA AAAGCCAAGA CTTCATCAAC TACATAGGTC TTACCATTGA	50
5	CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT	100
	AGAAAGGCAT CTTCGCCAG TGGATTGCC TCAAGGTTG	139

(2) INFORMATION FOR SEQ ID :631:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20	CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC	50
	TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA	100
25	GCTGAAGTGG TGTGCTT	117

(2) INFORMATION FOR SEQ ID :632:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

40	CCAGCNCCGA AAAGCCAAGA CTTCATGAAC TACATAGGTC TTACCATTGA	50
	CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT	100

325

AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTGA GGCGGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50

ACAAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC 50

35

TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150

40

GAAGATATGT ATGCAACGTT CATTCAAA 178

(2) INFORMATION FOR SEQ ID :635:

326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC

50

CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA

90

15

(2) INFORMATION FOR SEQ ID :636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG

50

GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC

100

30

T

101

(2) INFORMATION FOR SEQ ID :637:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

327

(xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50
5 TTTAATAAAAG CACAGCACAA 70

(2) INFORMATION FOR SEQ ID :638:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :638:

20 CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50
ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100
TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC 150
25 TCGGAGCTCG 160

(2) INFORMATION FOR SEQ ID :639:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :639:

40 CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50
CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC 100

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

(2) INFORMATION FOR SEQ ID :640:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15

CCGACCACCC CTTCTTTTC TTCGTCCATC CAGCACAGCA AGACCAAACGG

50

GATTCTCTTC TGCGGCCGCC ACCGCGTGGA

80

(2) INFORMATION FOR SEQ ID :641:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA

50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA

100

35

(2) INFORMATION FOR SEQ ID :642:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA

50

5

GTTAATGTTC CATCCATGCT GCTTAAA

77

(2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT

50

ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG

100

GGCTACAAGG ACTCGCCCTC CGTCTGG

127

25

(2) INFORMATION FOR SEQ ID :644:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

40 GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT

50

40

GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA

100

AAGTTTATTT TAGACC

116

330

(2) INFORMATION FOR SEQ ID :645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTCTG GGTTTCCAG	50
15 GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC	100
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATAACAAG	150
20 ACACCTCAAGA CAGCAATTAA TCTGTCATCA TT	182

20

(2) INFORMATION FOR SEQ ID :646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA	50
35 ATAAAAATCT GAAAAC	66

(2) INFORMATION FOR SEQ ID :647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTCCGA AGGATAAAAT 50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT 93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTG TCCCCACTGA GATGTATGAA GCTTTGGTC TCCCTGGGAG 50

25

TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA 100

AAAGTGCACA CCTT

114

(2) INFORMATION FOR SEQ ID :649:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG 50

332

GGATTCTCTT CTGGGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100
GTGTGACACC ACCGCATNNNT GATGACCGAT AATAAAAATA TAACTAATTT 150
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTTCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs

333

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

10	CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTA	50
	AGAAATTCCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT	100
	CTCGAGGACC TGGAAAGAAC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
15	TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198

(2) INFORMATION FOR SEQ ID :653:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 224 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

30	CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
	ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
	GCATCTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
35	TGAAAAAATTG CACTCCCTTG GTGTAGACAA TACCAAGTTCC ATTGGTGTG	200
	TTGCTATAAT AACACTTTTC TTTT	224

(2) INFORMATION FOR SEQ ID :654:

40

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 226 base pairs	

334

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

10	CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCGGGCAGT	50
	GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC	100
	CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA	150
15	AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTTGGTTT	200
	CTGAGCGCAT AAAGCTAAGG AGGGGT	226

(2) INFORMATION FOR SEQ ID :655:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 167 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

30	(xi) SEQUENCE DESCRIPTION: SEQ ID :655:	
	TTAAAAAAAT TCCCCCCTTT AATTGACCAA ACTAAAGCCA TGACATTTCA	50
	TTTGGTAACC TGTTTAGAAT TATAAAAATC ATTCATTTG GCCCAGCCCA	100
35	TACGCCAAG AGAAAACCTTC CAGACTTTTC TGATGCCATC CAGTTTGTT	150
	CTTACAAAAT GCATATT	167

(2) INFORMATION FOR SEQ ID :656:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

10	CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT	50
	TCTGCGGCCG CCACCGCGTG GA	72

(2) INFORMATION FOR SEQ ID :657:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

25	AGAGGGTTT CTATATGTAA TTCTTTATT CTGTAAAAGG TAACAAAATA	50
	TACAGAACAA AAAAACTTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA	100
	TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAT AAGGTGTATA	150
30	GTACAATGTA TTCTAAAATC GTTCCGCC	178

(2) INFORMATION FOR SEQ ID :658:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 76 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTTCCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

20 GCCAGCGCCG AGGTGCGATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
AACAAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAAACTTC TTTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50
TAATCCTTT CACTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100
40 AAACACTGAT CAAACTCAGT TGTCCTTACG TTAGCATTAC TCTGTCAAG 150
C 151

(2) INFORMATION FOR SEQ ID :661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :661:

	AGGCACTGAC CCCTGCCACC CCTCACTGCA TAACTTCAG CCACGCTCTCC	50
15	TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT	100
	CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG	150
	TGGGGCCTAT GATTGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC	200
20	TTCACTGTGC CTGCTGAGTC AGCTTGCATC TGCGCCTTCG GTGCG	245

(2) INFORMATION FOR SEQ ID :662:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :662:

35	GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
	AATAAAAACM TGAAAACACC CC	72

(2) INFORMATION FOR SEQ ID :663:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

338

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCCTAT CACTCTCCCC	50
10 AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88

(2) INFORMATION FOR SEQ ID :664:

15 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 223 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

25 GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA	50
GAACCTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC	100
30 CCCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG	150
CGCCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG	200
CGGATAGTCA CACTCCCTGC CGA	223

35 (2) INFORMATION FOR SEQ ID :665:

40 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 70 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAAACACC 70

(2) INFORMATION FOR SEQ ID :666:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCACC 100
TTTCTACGTA CCGTATAG 118
25

(2) INFORMATION FOR SEQ ID :667:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
35

(xi) SEQUENCE DESCRIPTION: SEQ ID :667:

40 GCCAGCGCCG ACGATGCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC 50
AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :668:

340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTAAA CTTGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

15

(2) INFORMATION FOR SEQ ID :669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :669:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCAA

50

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG

100

30

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC

150

GAGAAGGACA AAATCACCAAC CAGGACACTG AAGGCCCGAA TGGACTCGCC

200

35

CTGCTCCAG AGCCCACTTT TTT

223

(2) INFORMATION FOR SEQ ID :670:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

341

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :671:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35

GCCACCGCCG ACTCCAGGCA CTCACTAAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :673:

	GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTT	50
10	GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGG	100
	GTGAGGGGGT TACCCCTTCC CAGTGTTTT TATTTCCGTG GGGCTCACCC	150
15	CAAAGTATTA AAAGCAACTT TGCAATT	177

(2) INFORMATION FOR SEQ ID :674:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 77 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :674:

30	GCCTGCGCCG AGCACAAAGAC AATGACGAAC ATTTTAAAAA AAAAGAATGA	50
	CGCACATTT AATAAAGCAC AGCACAA	77

(2) INFORMATION FOR SEQ ID :675:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

	GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG	50
5	CCGTAACCTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC	100
	ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACACA CCGATTGCAT	150
	AAAATCTTTT TTTAGGAAAA AAACAC	176
10		

(2) INFORMATION FOR SEQ ID :676:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 141 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :676:

	GCCAGCGCCG ACGCCAGAG AATAACAGTAC TTAGGGGTTA CACACAACAG	50
25	CCGTAACCTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT	100
	ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C	141

(2) INFORMATION FOR SEQ ID :677:

30 (i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 365 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :677:

	CTCTGAACAG ACACGAAGCT GCCCCCTCGTA CAGCCACTCG GGCGCTGACC	50
--	---	----

344

	ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG AACTGCACG	100
	CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA	150
5	CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCAC GTGGACCTAG	200
	GTGACTGGGA GGCCACCAAG CAGGCACCTGG GCAGCGTGGG CCCCCTGGAC	250
	CTGCTGGAGA ACAACACCAAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT	300
10	CACCAAGGAG GCCTTCGACA GATCCTTGA GGTGAGCTTG CGTGCATCA	350
	TCCAGGTGCT GTAGA	365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

	GCCTGCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
	CAGGGAAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC	100
30	GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAAGCA GATCTTGACA	150
	GCCTTGCCCG CGAGTGCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG	200
35	TGACTGGGAG GCCACCAAGC AGGCACCTGGG GTAGCATGGG CCCCCTGGAC	250
	CTGCCGGAGA ACAATACCAAC CGCCGCCNTN GCCGCAGTCT TTCCCGGAGG	300
	TCACCAAGGA GGCTNTTGA TAGATCTTT GAGGTGAGCT TGCCTGCGGT	350
40	CATCTAGGTG CTGTAG	366

(2) INFORMATION FOR SEQ ID :679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :679:

	GCCTGCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
15	CAGGGAAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA	100
	GTCTGCAGCA GGCCCCTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC	150
	CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT	200
20	TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC	250
	TTG	253

25

(2) INFORMATION FOR SEQ ID :680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- 30 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :680:

	GCCAGGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG	50
	GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC	100
40	CCACACACCC TTCAGGAAGG GGGAGCACTG AGAACACAG CACAGGGCT	150

346

	CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA	200
	AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA	250
5	GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG CCTC	294

(2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 268 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :681:

20	CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGGCC CCGTGGCGC	50
	GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG	100
	CTTTTCAGT GGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC	150
25	TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC	200
	TGCCAACCCAG AACTGACACG CGACCTCCTG GGCCTGACG CCATTAAC	250
	CAACGTTGGC GCCCGGCG	268

30

(2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 354 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

347

	GCCACCGCCG AGGAAAACCG TGCACGTGTTA GCCATGATCA ACCCCACCGT	50
	SCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG	100
5	AGCTGTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA	150
	AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCTGCT TTCACAGAAT	200
	TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTCACACGC CATAATGGCA	250
10	CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC	300
	CTAAAGCATA CGGGCCCTGG CATCTTGCCT ATGGCAAATG CTGATCCTGA	350
15	TACA	354

(2) INFORMATION FOR SEQ ID :683:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 148 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :683:

	CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCT CTCCTCTCTG	50
30	TCCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC	100
	AGTGGCGGCA GTTCAGAAAT AAAGGGCCA TTTGCGGGAT GCCGCATT	148

35 (2) INFORMATION FOR SEQ ID :684:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 307 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :684:

	AGCACCGAGG CGCTCAAGGT CCTGGGAAAC CCCAAGAGCG ACGAGACGAA	50
5	CGCGAAGGCG CTGGACTTTG AGCACTTCT GCCCATGCTG CAGACAGTGG	100
	CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG	150
10	GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGCGCTG AAACCCGGCA	200
	TGCTCTGCC ACACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC	250
	TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAACCATTT	300
15	GTGAGGC	307

(2) INFORMATION FOR SEQ ID :685:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 174 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30	CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGAAACGT ATGCTAGCAG	50
	AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCCTCTT AGCTGGCAAA	100
	TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA	150
35	GGAGCCATCT CTAGCGGGCC CTTC	174

(2) INFORMATION FOR SEQ ID :686:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 106 base pairs
	(B) TYPE: nucleic acid

349

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACAC AGTAATCACA	50
10 CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTACT	100
TATAAA	106

15 (2) INFORMATION FOR SEQ ID :687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTTCCCCA	50
30 GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAAACCC AAAACCA	97

30 (2) INFORMATION FOR SEQ ID :688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCCTCCT GCCCACTGGA 100
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150
GAATAGAGTC TAAGCGAACG AC 172

(2) INFORMATION FOR SEQ ID :689:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20 GCCACCGCCG AGCTCACCCC TGCGGTGCAC GCCTTCCTTG GACAAGTTT 50
TGGCTTCTGC GAGCCTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCCTCC 150
CTCCTTGAAC CAGCCCTTCC TGGCCTTGA ATAAAGTTA AGCGAGTAGC 200

(2) INFORMATION FOR SEQ ID :690:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40 GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTGA ATGCGGCCCA 50

351

ACACAAATTCA ACAAGTGNTC TCAAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15 TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA 50
TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG 100
TAACAGGGAT ATGAGCTCTA GCCGCCAAG CTAGCAATGG CAACCCTTCT 150
20 GGGTCCCCCTT TCAGCATGCG GAAGCTTTTC TTCCACTTCA CTCCATAAAC 200
AGCTGACGCT CAAAAAG 217

25 (2) INFORMATION FOR SEQ ID :692:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCCTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCAAGGGGA 50
GAAGAGTAAG AGACAGCTTT CA 72

40 (2) INFORMATION FOR SEQ ID :693:

352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG	CCCGCAAGCA	GAGGGACTCG	GAGATCATGC	AGGGGAAGCA	50	
GAAAAAAGGCA AACAAAGAAGA AGGAGGAACC CAAGCAGCTT TGCGGCTTCG					100	
15	CGTCCAACCC	TCTTGCCCTT	CACCTACGCG	CCTAGAGCCA	GTCCCACAC	150
GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTC					200	
CCTTTGACCT AAGCCTACAG CAGGCCCTT TTGTGCTTCC TTCCCCTCAG					250	
20	GCAGCCTCTT	TCCCCCTGGG	CCACTCCCAG	GGGTGAGGGGG	GTTGTCCCTTC	300
CCGATGCTTT TTGTTACCGT GGGGTTTGC					329	

25

(2) INFORMATION FOR SEQ ID :694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :694:

40

TCTGCTGCCG	CCCGCAAGCA	GAGGGACTCG	GAGATCATGG	CCTGCCCGA	50
ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCCA CACGGATCCG					100
GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGCGGACCA					150

353

	GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA	200
	AAATCACCAAC CAGGACACTG AAGGCCCGAA TGGACTAACCC CTGTTCCCAG	250
5	AGCCCACCTTT TTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG	296

(2) INFORMATION FOR SEQ ID :695:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :695:

20	GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCAACCTAA GCCCCTAAGG	50
	AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG	100
	CGTGTCTTAG CACTAACCTC CTCCCTAGCC CCTTATTTGG TGGCAGAAGT	150
25	GGCCTCCACC CCTTCACCGT TTAAAAATAC TCCGTGGAGA AAAGAAAGCT	200
	TNAAGGAGTA G	211

30

(2) INFORMATION FOR SEQ ID :696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :696:

40

	GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC	50
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354

CCAACAAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

(2) INFORMATION FOR SEQ ID :697:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15

GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC

50

CTACCAGCAA GGGGTCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG

100

GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCCTTGC GCTGATGGCC

150

20

ATAGTCAAGA GAAAGGATTG CTGAAGGCAG CCCTAGAACG GGAGTTAGGA

200

GCTTCTAACCG CGTCATGGTT TAAATACACA CCCTTTTTG GACAGCGCTT

250

25

CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCTATGC

300

GCATGCGTAC CTGT

314

(2) INFORMATION FOR SEQ ID :698:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40

GCCACCGCCG AGTTCACCCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT

50

355

GGCTTCTGTG	AGCACCGTGC	TGACCTCCAA	ACACCGTTAA	GCTGGAGCCT	100	
CGGTAGCCGT	TCCTCCTGCC	CACTGGACTC	CCAACAGGCC	CTCCTCCCC	150	
5	CCTTGCACCG	GCCCTTCCTG	GTCTTGAAAT	AAAGTCTAAG	CGGGCAGC	198

(2) INFORMATION FOR SEQ ID :699:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 230 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

20	GCCAGCACCG	ACAGCAACAA	AAATGTTCCC	ACAGAGATCA	GGATGACTTG	50
	CTGAAGCTCA	GTGGAGGCTA	AAAAGAGGAC	ACAAAAGTGA	ACAGAATGAC	100
	CTTCCTACGC	ACAACACAAA	CACCAAGTTAA	TGCTCCATCC	ACGCTGCTTA	150
25	AAGAGCATTG	CTGTCCCTAGC	AAAATGGGCA	AGTCCCTCTA	CCCCCCACCC	200
	TTAGCCGGCA	TGCTTACATT	AATAGCTAGA			230

(2) INFORMATION FOR SEQ ID :700:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 282 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

40	(xi) SEQUENCE DESCRIPTION: SEQ ID :700:	AGCAACAAAA	ATGTTCCAC	GGAGATCAGG	ATGACTTGCT	GAAGCTCAGT	50
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356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC	100
AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCCT	150
5 GTCCTAGCAA AATGGCAAG TCCCTCTACC CCCCACCCCTC ACTTGGCATG	200
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA	250
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC	282

10

(2) INFORMATION FOR SEQ ID :701:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCAA	50
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG	100
CTCGGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC	150
GAGAAGGACA AAATCACCAAC CAGGACACTG AAGGCCGAA TGGACTAACCC	200
30 CTGTTCCCAAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC	250
TTTCG	255

35

(2) INFORMATION FOR SEQ ID :702:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA 50
CGCACATTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCCGCTA 50
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCA 50
ACACGGATCC GAATCACCTG GCCCCAAACC ACCTACCTAG CCATGATGAA 100
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10	GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG	50
	ACGCCAACCA CGGATCCCGA TCACCTATCT GAAACCATCT CCCAAGCCAT	100
15	GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCC	150
	ACATCACCGA GAAGGGACAAA ATCACCAACCA GGACACTGAA GGCCCCAATG	200
	GACTAACCT GTTCCCAGAG CCCACTTTT TTCTTTTCA GAAATAAAAC	250
20	AGCCTGTCTT TC	262

(2) INFORMATION FOR SEQ ID :706:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35	GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCAACCTGA GCCCCTGAGG	50
	AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG	100
	CGTGTCTTAG CACTGCCCGC CTCCCTAGCC CCTTATTGAG CGGCGGAAGC	150
40	GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT	200

TCAGGGAGT

209

(2) INFORMATION FOR SEQ ID :707:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15	GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC	50
	TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAAGA AGAAGGAGGA	100
	ACCCAAGCAG CTTTGCAGCT TCACGCCAA CCCTCTCGCC CTTCACCTGT	150
20	GAGCCTGGAG CCAGTCCCAC	170

(2) INFORMATION FOR SEQ ID :708:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35	GCCACCGTCG AGGATTCAAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG	50
	ACGTTCCGTT TCCCCCTGCC CGCCTTTTC CGCCACCAACCC GCGGCCGCT	100
	TCTGCAGGCC GTTTCCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA	150
40	CCCAGAACCT	160

360

(2) INFORMATION FOR SEQ ID :709:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAAACT GCAAACTCCT

50

15

G

51

(2) INFORMATION FOR SEQ ID :710:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA

50

30

CAGGATTCTC TTCT

64

(2) INFORMATION FOR SEQ ID :711:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

	CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTT CCCATCTTCT	50
5	CTCTCTTGGG TGATGTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC	100
	TGGG	104

(2) INFORMATION FOR SEQ ID :712:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 68 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20	CTAGAAATAG ACCCACAAATT TAGAGACAAT CTATACTAGA TTTATCTCCT	50
	TTGTTTTAG TTGAAGGC	68

(2) INFORMATION FOR SEQ ID :713:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 127 base pairs
	(B) TYPE: nucleic acid
30	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

	AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT	50
	GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT	100
40	GTGCTTGGGT CGCTGTCTAC TGCTCCT	127

362

(2) INFORMATION FOR SEQ ID :714:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC

50

15

CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATT

90

(2) INFORMATION FOR SEQ ID :715:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA

50

30

ACAAAAATCT GAAAACATC

69

(2) INFORMATION FOR SEQ ID :716:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

	GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA	50
5	CCACCAACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT	100
	AA	102

(2) INFORMATION FOR SEQ ID :717:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 124 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20	AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT	50
	GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT	100
25	GTGCTTGGGA TACGCTGTCT ACAG	124

(2) INFORMATION FOR SEQ ID :718:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 123 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

40	GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA	50
	TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCCTTGAG CTGTTTGCAG	100

364

ACAAGGTCCC AAAGACAGCA GAA

123

(2) INFORMATION FOR SEQ ID :719:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC

50

TTCT

54

(2) INFORMATION FOR SEQ ID :720:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTTGTTT TCAACAGTCT TGCTGAATT

50

AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGCAG ATATAGCATT

100

35

AATAAAACTG TGCACTC

117

(2) INFORMATION FOR SEQ ID :721:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25

ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCAGG TGCAGGTATA TGATTGCCAT ATAATAAAAAA TCTGAAAACA 50

40

TCCCC 55

366

(2) INFORMATION FOR SEQ ID :724:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :724:

	GTGTACTATT AGCCATGGTC AACCCCACCG TGTTCTTCGA CATTGCCGTC	50
15	GACGGGCGAG CCCTTGGCGC GCGTCCTTG AGCTGTTGC AGACAAGGTC	100
	CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
	TTTGGTTATA AGGG	164

20

(2) INFORMATION FOR SEQ ID :725:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :725:

	GTGAGAACCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC	50
35	ACACCCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC	100
	AAGTTCAAGTA	110

40

(2) INFORMATION FOR SEQ ID :725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :726:

	CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTCTTC GACATTGCCG	50
10	TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG	100
	TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
15	TTTGGTTATA AGG	163

(2) INFORMATION FOR SEQ ID :727:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 105 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :727:

	GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
30	GTCACTGGGG AAAGCAGGGA ACCAGTGTGA ACTCTTTATT CACTCCCAGC	100
	CTGTT	105

35 (2) INFORMATION FOR SEQ ID :728:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 186 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :728:

	GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG	50
5	ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCC	100
	AGGAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTCGA GGCGCCACT	150
10	GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA	186

(2) INFORMATION FOR SEQ ID :729:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 167 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :729:

	GCCAGCGCCG AGGTTGCATA TTCTAGGCCG AGGTATATGA TTGCCATATA	50
25	ATAAAAACCT GAAAACATCC CACCCGGGAA AAAAAAAA AAAAAAAA	100
	AAAAACACCC CCCCCCCACA AAAAACTCAA ATTCCCCTCC CAAAAAACCC	150
30	CCTCAAAATC AAAAAAC	167

(2) INFORMATION FOR SEQ ID :730:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 64 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA

50

CAGGATTCTC TTCT

64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCCTGGC GGCTACCGG CCCCCCGTGC ACCCCCGCTA

50

GCGCCCCACC CCGCGTCTAT CGCCAATAA AGGCATCTTT GCCGGG

96

20 (2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA

50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA

84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAAG CCCTCCGTGC ACCCCCCGCTA 50

25

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAAG CTCCCTCAGTG CACCCCCACT 50

40

AGCACCCCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG 97

371

(2) INFORMATION FOR SEQ ID :736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :736:

	GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT	50
15	GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA	100
	TACAGCATTA ACAAAACCGC GCATCTC	127

20

(2) INFORMATION FOR SEQ ID :737:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :737:

	GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA	50
	CAGGATTCTC TTCT	64

35

(2) INFORMATION FOR SEQ ID :738:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

GCCAGCGCCG ACAATGCCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50

5

AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :739:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG 50

CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCAATCTTG CCGGG 95

(2) INFORMATION FOR SEQ ID :740:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35

GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA 50

GATGAATGAG AAGATGCCGA ACTTGCGCA CTCCATGCC CTGCTGCAGA 100

40

CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTGAAAGGA 150

CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT 200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

(2) INFORMATION FOR SEQ ID :741:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15 GCCTGCGCCG ACGATGCCA GAATCCAGAA CTTCGTCTAT CACTCTCCCC 50

AACAAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG

88

(2) INFORMATION FOR SEQ ID :742:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAAATATTC 50

GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA 100

35

CTCTGATAGT CTTCATTCCG ATAGACTAAA GCGTGTGCTG ACTGGAGATG 150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT 200

40

CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA 242

(2) INFORMATION FOR SEQ ID :743:

374

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

(2) INFORMATION FOR SEQ ID :744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :744:

25

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

(2) INFORMATION FOR SEQ ID :745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :745:

40

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT

50

AATAAAAATC TGAAAACATC CCAC

74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC

50

AACAAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG

88

20

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC

50

35

AACAAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG

88

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

	GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTT	50
	GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG	100
10	GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC	150
	CAAAGCATTA AAAGCAGCTT TGCAATT	178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 235 base pairs
	(B) TYPE: nucleic acid
20	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

	GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG	50
	ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCC	100
30	AGAAAGGCAT CTTCGCCAG TGGATTGCC CCAAGGTTGA GGCGGCCATT	150
	GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCC	200
35	TGGCGCTGCT GCCTATAACA AACACTTTT TTTTT	235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 87 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTC ATCCAGAAAA GCAAGAGAAA

50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT

87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCTGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG

50

25

GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC

100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC

150

ATGCCAAAGA CACTCAAAGA

170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT

50

AATAAAAAAA TGAAAACACC CC

72

5 (2) INFORMATION FOR SEQ ID :753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTG GACAGCGTGG GCATCGAGGC

50

GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAAACA

100

20 TTGAAGACGT TATTGNCCAG GA

122

(2) INFORMATION FOR SEQ ID :754:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACCGCCG ACTGAAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA

50

GGTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC

100

AGGCGCCACC TTCACCTGGA CACCCCTCAAG CGGGAAGAGC ACTGTTCAAG

150

40

GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG

200

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

(2) INFORMATION FOR SEQ ID :755:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT

50

AACAAAAAACC TGAAAGCATC A

71

(2) INFORMATION FOR SEQ ID :756:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30

GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

35

TAGTGCTTT TCAGTGGGGC GGGGCGGGAA GCAGGGCGGG A CCAGGCAGCC

150

AGTTCTCAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGCGC TGA

243

40

(2) INFORMATION FOR SEQ ID :757:

380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA

50

CAGGATTCTC TTCC

64

15

(2) INFORMATION FOR SEQ ID :758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCAGGGAA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

35

GACGTCGACA ACCAGAACTG ACGTGCGACC TCCCGGGCGC CGA

243

(2) INFORMATION FOR SEQ ID :759:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

	GCCACACCAAG ACTTCGACC CCCCAACCCCT CTGAGGAAGA TGGGGGCAAG	50
	AAGATCACGC TCCCCGCCTG TTCCCCGCC GCTTTCTCC TCTCTCTCT	100
10	CTTCGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG	150
	TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA	200
15	TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTC GGCCA	245

(2) INFORMATION FOR SEQ ID :760:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 68 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

	GCCAGCGCCG AGGTGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT	50
30	AACAAAAAACC NTGAAAAC	68

(2) INFORMATION FOR SEQ ID :761:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 71 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

50
GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
5 AATAAAAAC GAAAACACCC C 71

(2) INFORMATION FOR SEQ ID :762:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :762:

50
GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50
20 AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :763:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :763:

700
35 GCCTGCGCCG ACAAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA 50
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100
400
40 CCCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150
CGCCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCCGTG 200

383

CGGATAGTCA CACTCCCTGC CGA

223

(2) INFORMATION FOR SEQ ID :764:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAAACACC 70

(2) INFORMATION FOR SEQ ID :765:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30 GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCCACC 100
35 TTTCTACGTA CCGTATAG 118

(2) INFORMATION FOR SEQ ID :766:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC

50

AACAAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG

88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT

50

25

ACAAGCAGAA GCAATAAACCC AATCTGATTT TCTTTTCAAT T

91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCAA

50

40

CATGGATCCG GATCACCTGT TTGAAACCCT CTCCCAAGCC ATGCTGAATG

100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCAC TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35

(2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTCAA CTCGATCTTC AACTCTGCAT 50
5 ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :772:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTT 50
 GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCGGGG 100
 GTGAGGGGGT TACCCCTTCC CAGTGTTTT TATTTCCGTG GGGCTCACCC 150
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

(2) INFORMATION FOR SEQ ID :773:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40 AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50

387

	GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC	100
	TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG	150
5	T	151

(2) INFORMATION FOR SEQ ID :774:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :774:

	ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTCAAA CAGTGAACCA	50
20	CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA	100
	CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC	150
25	ACTATGGAGC ACACAACCTCT GCCTCGCGCT GACACCAGAC AAACACGGCG	200
	GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG	250
	AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA	299

30

(2) INFORMATION FOR SEQ ID :775:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

	TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTGCCATTG	50
	TGGCGTAATT TTCTGTGCCGA GTGAATGTGG CGCAAACAAAC TATATATCNA	100
5	AACCGTATAT TTAAAATGAA TTACTAGAGA GGGAAATGTAA TCATGGCAAA	150
	AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC	185

(2) INFORMATION FOR SEQ ID : 776:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 255 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID : 776:	
	ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA	50
	TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC	100
25	ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA	150
	AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT	200
	CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC	250
30	AACAT	255

(2) INFORMATION FOR SEQ ID : 777:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 239 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

389

(xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAAAATTCTG TTCTTGGCTG AATCGTGTAA	100
	AACCGTTGTA CACAACGTAG TAAAATTCTAT AACCCATCTG CATAACCAATC	150
	GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

(2) INFORMATION FOR SEQ ID :778:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 252 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAAGTTG GTATTGTTTG AAGCAGCCCCA ACAATTTCGA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTTAAGG ATGACTCAAC TTCCGCCAACT CGGTTCCCTCA TTAGGACAAAC	250
35	TA	252

(2) INFORMATION FOR SEQ ID :779:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

	TCGGATTATACGGCTGTTA GTGCTATCGG CGTCTGGTAT GTGTTATATA	50
	TCGCCTATCG TTTTTGGCC AATGGCGTT GGCTACGCGG GGCAATGATT	100
10	GCCATCGTT TTGTTATCTT GACTTATTTC GTCATTTAA ATATTATTTA	150
	ACTATTTAC AAATAAAAGTG GTCAAATGGG ATATTTGCC AAAAATAGAG	200
15	AAAGTGTAG GCGGCCACA GCTGGAGGAA GAGAAAGCGG CTGTGCATGA	250
	AGTTATTGCA CCCGC	265

(2) INFORMATION FOR SEQ ID :780:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 249 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :780:

	CTCAGCTGGA CCAAATTAGT TGAATTACTC ACCATCAATA AACTATAAAT	50
	GGCGCCAATG ACCAACCCGC CAACGATTCC CGTTGTCAA GAACCTAATA	100
35	ACAAGTAACC AACCGCAGCC CCAACAAGCC CAACTAGGTT TAAAAAAACC	150
	AAGCAAAAGG CCAACTGTCC GTCGTTTATT GGATTGTATC TGCTCATATA	200
	ACATTAAAAC TTAACCGTTG GCACTTCTTT CTCAGACCCG CCGATACTG	249

40 (2) INFORMATION FOR SEQ ID :781:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID :781:
GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG 50
CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCC 100
15 TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150
TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA 188

20 (2) INFORMATION FOR SEQ ID :782:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :782:
AATATTTATT TCATTTGTTT ACTACCACCT CATTATTTATTT GTTTGCTGCT 50
GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGAACTTT TGTGGCTCC 100
35 AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTTGG AACATCTAAC 150
AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT 182

40 (2) INFORMATION FOR SEQ ID :783:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs

392

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

	CACAGCCAGA GCTTCGTCTT CAGTGACCAAC AGGGCTGAGC CAGGCTCAAC	50
10	CGGCTTCTGG CTCTTGTCTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT	100
	CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT	150
15	TTCCCTGAGTT CCTGACCCCT GCTATTTAT TAGTCAGCTC TCAGCACTTA	200
	CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG	250
20	AGAGAATTCA AATGCGTGTT GGTGTTCTG TTAGTACAAG CAGCA	295

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

	CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC	50
35	GTGTGTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCACT TCAGAACCG	100
	TACCTGATGT TGTTGGAATG GCAACCATT GTGTCAAACG CACTGGTAGA	150
	ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTGTTC TATTTCCATG	200
40	AACAATTCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT	250

393

TGAGTATTG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

(2) INFORMATION FOR SEQ ID : 785:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 785:

15	GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA	50
	CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTC	100
	ATTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC	150
20	CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAAA	200
	GCGCTTGAA TACTGTTCTG GGTCACGGT GGAGATCTCC GCGCAGCCAT	250
25	GTTAACAGT TTTGCAGCA TGGCAGCTT TCTTTTTGC ATCATAATGA	300
	GTA	303

(2) INFORMATION FOR SEQ ID : 786:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 786:

40

TATGGCCCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT

50

394

	CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTGACG ACTGCTTCAT	100
	ACATGAAGAA TGATGGTGT CGTGGGCCA TTAAGTACTA AGCCAAGAAG	150
5	TTATCACCGAC AACCTATAAC TTGGGCCGAA TTAACTTGAT GATGCACGGG	200
	GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA	250
	CTGGC	255

10

(2) INFORMATION FOR SEQ ID : 787:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 206 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID : 787:

	CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG	50
25	TCAGAATCAA CAAAACCTAGG TTGGTTAAC ATATCTCTGG TACATCAAGG	100
	GGCATGATAC AAACCAGTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG	150
	ACTTATTTTT ATTTTTTTT TTTTGGACAG ACTCCCTTG TCCCCAGGCC	200
30	GGAGTG	206

(2) INFORMATION FOR SEQ ID : 788:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

395

(xi) SEQUENCE DESCRIPTION: SEQ ID :788:

	ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT	50
5	CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCGAG	100
	TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTCAAAC GAGGCCTGGA	150
	AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG	200
10	GAACAATTCC GCGACACCCCT TCGTCTGACA AAAAACCTTC GTGACGCGTC	250
	GAGTATCCGC	260

15 (2) INFORMATION FOR SEQ ID :789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

	AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAAACGT CAAGGCCGCC	50
	TGGGGTAAGG TCGGCCTGCG CACTATGCCGT GAGTATGATG CAGAGGCCCT	100
30	GGAGAGGATG TTCCTGTCCT TCCCCACAC CAAGCCCTAC TTCCCGCACT	150
	TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG	200
35	ATCGACGC	208

(2) INFORMATION FOR SEQ ID :790:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

	AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT	50
	GAAAATACAT TGTTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC	100
10	ACTCTTGCTA TCGACCACATCG TCGCGCTTTG GATGAACCGT CGTAAGTCAC	150
	AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT	200
15	TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG	250
	TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC	289

(2) INFORMATION FOR SEQ ID :791:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 232 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

	TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAATT TGGCAATTAA	50
	TTGCTCATTA TTAATGGTAG AGTTTCATT AATGAAGTTG GAAAATACGG	100
35	TGAATCTTTC AATGAACCTCA GTTAGACATT CGGAATGAGC TTCATACATT	150
	GTCTTATTAT CTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAAA	200
	CCAAATTGAA GCACCTTATC TATGATCCGG GC	232

40 (2) INFORMATION FOR SEQ ID :792:

397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC	50
TGGTAATATC GAACAAACTA TTTTAAGAA CTTGATTCT GGCAACATTA	100
15 AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG	150
GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA	200
TGCCTATTC GCGAAGTATG GATCTAAATA AC	232

20

(2) INFORMATION FOR SEQ ID :793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTCACGGTA GTGANCCAG TGACCAGATG TCTTATACAA	50
35 GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA	100
ATTCTTGTC GGTGATGTA CGTTCAACTT GACGGCGAAG CGATTGCC	150
ATTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA	200
40 ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTACGTTT TTTAGCTTCT	250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

(2) INFORMATION FOR SEQ ID :794:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15	CAGCAGGCAC AACACCATCG GTTGTGCGCTG AAAGTATTTT TAAAGTCTTTG	50
	GCCAAGAAAGT CAGTTTCAGC TAAGTTAGAC GGCACTTATG CGGGTATGCA	100
	TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG	150
20	ATGAAGCGTC GAATTCTGTCG CGTCATTCTG CCTCACACTC ACAGGGCACAA	200
	GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC	250
25	CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC	288

(2) INFORMATION FOR SEQ ID :795:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :795:

40	GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT	50
	CGATAGACCC AAAAAGTGT TTAACCTGGAA AACACCTTAT GAGGTTTATT	100

399

	TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT	150
	CTCAATCACCA GCATTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC	200
5	GAGGTCAGTT ACGGCGTCCA GTCTTGAGC AGATGATTG CCCCGAGTGA	250
	TCGTCGGC	258

(2) INFORMATION FOR SEQ ID :796:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :796:

	TGCTTCAAAG CCTGGCTTAA CCCGCTTGCC CACCAACTTC AATTATACCT	50
	GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC	100
25	CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACCA TTTAACACAC	150
	AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG	200
	AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAAGGAC TAGCGGTACG	250
30	CTCATGTAAC GCGACAATAT	270

(2) INFORMATION FOR SEQ ID :797:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

400

(xi) SEQUENCE DESCRIPTION: SEQ ID : 797:

	AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC	50
5	TTGTGTAGGT TGTCTGAAAC GGTCGCAGTC ACCGGTTAGC TTGATAAGTC	100
	AGGTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC	150
	AATCGCAGTT TACATCATTA AGACCCTTAC TAGAAGTAAC TGGCCATCCT	200
10		
	GCCACCGCTT	210

(2) INFORMATION FOR SEQ ID : 798:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		

(xi) SEQUENCE DESCRIPTION: SEQ ID : 798:

25	ATCATAAGCG CTGGAACCTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT	50
	GTТАGCCCCA AGAGTCTACA CTCTGCCAAT GGTGGCGCTCC ATAGGAAAAAA	100
	CCACGGTCCA AGGCAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA	150
30		
	TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCAAA TAACGAGACA	200
	ACTAGTTGAG CTAATGCG	218

(2) INFORMATION FOR SEQ ID : 799:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 176 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :799:

	CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCAGA CGTAGAGCTG	50
5	AGAATAGCAT TACCAAATGG AACAACGTGC TACAGTCAGG ATTAAAAAGA	100
	ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG	150
10	AACAATACAA CACTGAATTA CTCGGC	176

(2) INFORMATION FOR SEQ ID :800:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :800:

	GCAATTGCTT AATTGTTCT TCCTTCTTAG CATTGCTG AGAAGCCAAA	50
25	CGTTGCGCCA ATTCAAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA	100
	TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT	150
30	TTAGGAAGTG ACGGTCTGG GATACCCACAA TCACTAGGTT CGGGAAATCA	200
	GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT	250
	TCGA	254

35

(2) INFORMATION FOR SEQ ID :801:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 203 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

402

(xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5	ATCCAGGCC C ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA	50
	TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT	100
	AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATAACAAAT	150
10	AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA	200
	ATG	203

15 (2) INFORMATION FOR SEQ ID :802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

	GACACAACTG TGTTCACTAG CAACCTCAAA CAGACACCAT GGTGCACCTG	50
	ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG	100
30	GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG	150
	GACCCAGAGG TTCTTGAGT CCTTGAGGA TCTGTCAACT TCC	193

35 (2) INFORMATION FOR SEQ ID :803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

403

(xi) SEQUENCE DESCRIPTION: SEQ ID :803:

	AACAAAAGTT GAAAATTTA AATGGTCTTT TTATGGTTG CGTGACCTAA	50
5	AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC	100
	AATAGCGTAC AGATTTTCC GCATTAATCC GTGTTATAT TAACAGATT	150
10	GTAAAGTATC GTTAAAAAG GGAGAGAGGG GATAACCCTCT CTCTAGATAA	200
	ATGGGTCAATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTTCTAAA	250
	CGATAACAAG AACCCCAGTA GGTAGTATAG CAGTCTTAA	290
15		

(2) INFORMATION FOR SEQ ID :804:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 256 base pairs
20	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25	(xi) SEQUENCE DESCRIPTION: SEQ ID :804:
----	---

	AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA	50
30	ACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC	100
	AACATTTCCG GCAATTCTA CAGAAACAAG TTGAAGTACC TGACTTCCT	150
	CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCTAC CACTTCCGG	200
35	CCCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA	250
	ACAGGG	256

40 (2) INFORMATION FOR SEQ ID :805:

(i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAAGTCT	50
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGCGCG	100
	AGGCCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC AGAGATTCTT	150
15	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG GGCAACCTA	200
	AGACGAAGGC TCATGGCAAG AAAGTGTTCG GTGCCTTTAG TGATGACCTG	250
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286

(2) INFORMATION FOR SEQ ID :806:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 291 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :806:

	TTCTTCATCA GATTTACAT CTGCCTGATT AGAATCTTCT ACACTGGCCT	50
35	CAGAAGATGA TTGTTCAAAA CTTTTCTAA GTGCTGTAA AAAAACCTCC	100
	ACGGACAAAG TAAAATGCAG TTCTTATCG TTTAGCCAGT GTACAACAAA	150
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAAG ACTCAGAGAT GTAATAGATG	200
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC AATATGAAAG	250

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

(2) INFORMATION FOR SEQ ID :807:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15	AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTTATTAG GCAGAATCCA	50
	GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG	100
	GAACAAAGGA ACCTTTAACCA GAAATAGAAC AACAAAGAAAG CGAACTTAGC	150
20	GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAAC TTTACGATAG	200
	GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC	250
25	ACAGACCAGC ACGTCGCCA GGAGCC	276

(2) INFORMATION FOR SEQ ID :808:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :808:

40	GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT	50
	CGATTCTAAA TAGACCTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA	100

406

	ACATCGCTAG CTAATTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG	150
	AAGCTTGTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG	200
5	ACGTGATCGC TTATCGTA	218

(2) INFORMATION FOR SEQ ID :809:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :809:

20	AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA	50
	CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT	100
	TACTGCCCTG TGGGCAAAGG CGAACCGCGGA TGAAGTCGGC GGCGAGGCC	150
25	TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC	200
	TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG	250
	ACTAATGGCA AGCAAGTGCT AGACGC	276

30

(2) INFORMATION FOR SEQ ID :810:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

	GACTCCACCT GAACGGGCC CTTCTGAACC GCCTCTGTGG GAGCAGGGCCC	50
	CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCCCTCT	100
5	GAGGAGGCTT ACTGCTTTTC TTACTCGATT TATTTTCAG AGTTTTCTTC	150
	TTCGTACTTT TTTTAACGCA ACTATTTGCA TTTTTATTCT CCTCCATTT	199

(2) INFORMATION FOR SEQ ID :811:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :811:	
	AAACAGGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCCAAAA	50
	AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC	100
25	TGGGGGGCTT GGCGTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA	150
	GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT	200
	TGCACCCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT	250
30	AAGT	254

(2) INFORMATION FOR SEQ ID :812:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 284 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

408

(xi) SEQUENCE DESCRIPTION: SEQ ID :812:

	TTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA	50
5	CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA	100
	CCAAAGGACC CTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA	150
	CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCACTTC CAAACAGGCA	200
10	ACCTGCACCG GAGGGGAGAC TTTTCGCCA AAGCGACGGG CCAGCACACA	250
	GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA	284

15 (2) INFORMATION FOR SEQ ID :813:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 279 base pairs
	(B) TYPE: nucleic acid
20	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

	ATACAACAGC AGAAACAGGT ATCCACGGCAC AGTCCAGCAA CATTCTTCT	50
	GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA	100
30	GGCAAGGATG CTAACTCGAA GTCAATCACG CGAGTGATGT CATTACAAAC	150
	CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG	200
35	CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAG AGCTAGACGA	250
	CTGACGAAAC CTGAGAACCC CGAAGGACT	279

40 (2) INFORMATION FOR SEQ ID :814:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 208 base pairs
--	----------------------------

409

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10	AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCA	50
	CCAGTGCA	
	GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA	100
	CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC ACTGGCGACG	150
15	GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC	200
	AGCAGCCA	208

(2) INFORMATION FOR SEQ ID :815:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

30	(xi) SEQUENCE DESCRIPTION: SEQ ID :815:	
	AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG	50
	CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG	100
35	TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC	150
	AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA	192

(2) INFORMATION FOR SEQ ID :816:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 264 base pairs	

410

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :816:

	GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG	50
10	CCGCCTGGGG TAAGGTAGGC GCGCACAAATG GCGAGTATGG TCGCAGAGGC	100
	CCTGGAAAGG ATGCTCCGTG CCTTCCCCAC CATGTGAGAC CTACTCCACA	150
15	CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG	200
	GTGCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCAAC	250
	GCGCTGTCCC CCTG	264
20		

(2) INFORMATION FOR SEQ ID :817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :817:

	ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAA	50
35	AAAACCACTC AACAAAGCAAA CAACCCATCC TGTTTCATA ACGTTATCGT	100
	AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA	150
	AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA	200
40	TG	202

411

(2) INFORMATION FOR SEQ ID :818:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :818:

	AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA	50
15	TGTATTTACA TTCACAGAGA TCTTTATTAA TTTACAAGCG CTTTGAGTTA	100
	CTGTATAGTT TTTTTAAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC	150
	CCCATAGGAT AGGTAATGAA CTTTTTGT	179

20

(2) INFORMATION FOR SEQ ID :819:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :819:

	TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT	50
35	AATAGCATAG GAGCATTAA TAATACGATT CGATACAAAA AAGAATTAA	100
	GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT	150
	CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAACTG GATCAAGTTG	200
40	TACGCGGGTC CACGAAGTGA CAGACGAAAA ATGAAACGCAA GCTGATGTAA	250

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15	ACTCGGCACT TTCTTAGAAT AGACAATTTG CAAAATGTCC ATCCCAGGTT	50
	CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG	100
	TGAACTTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC	150
20	ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC	200
	TTTCCGTAAC TGAGTTTGAT TTCTCC	226

25 (2) INFORMATION FOR SEQ ID :821:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

30	CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTT TGGTTGTAAA	50
	TTTCAAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA	100
40	GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC	150

413

GTGATTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

(2) INFORMATION FOR SEQ ID :822:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15	GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTAT AGCTAGCAGG	50
	GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG	100
	GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT	150
20	TGCGCTTTCT TCATCGCAAC CTTTGCCAA GACATCTGTT TTTCTGGAT	200
	CACCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT	250
25	AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA	300
	CATG	304

(2) INFORMATION FOR SEQ ID :823:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG

50

414

	GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG	100
	CACCAANGGG GCGAACTCNC GGGGAGGCAGG GCGACCAGGG TCACCAGCAG	150
5	GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG	197

(2) INFORMATION FOR SEQ ID :824:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 281 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20	AAAAACAATG TCATTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA	50
	CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT	100
	GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCTGACT TACCCCTGGCA	150
25	GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA	200
	TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCAG ACAGCAAGCG	250
30	TTTTCCCACA GGCTCTGACA CACAGAAGAT A	281

(2) INFORMATION FOR SEQ ID :825:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 312 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

	TATTAATTT ACTAGAATGT TACAGTTACA AATTTGGTAA TGTTCTTCT	50
	GAAAAACAGC CTAATTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC	100
5	TTTTATTCAT GATAGAAAAA TAATTCTGG CTTCATCTCA CAATTAAC	150
	ATAATTATGT TAATATAAAA TATAACTGTG CCCTTCTTT TCAGTGATGA	200
	TCAAAGTGAT TCTCCCAGGC CAAAAAATCA AATAAGAAGT TATATTTAA	250
10	AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT	300
	CTACTAATTG GC	312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

	ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA	50
	GGGCAGGGAG GGGAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA	100
30	TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCC CCGGGTCTCA	150
	GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA	189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :827:

	CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT	50
5	ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAAG CTATGAGTAA	100
	AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT	150
10	TTAGAGATTA TTTTGTGCC TGGAAATCTG TCTCATCACA GAGTGTAAAT	200
	ATACACCGGC GGGATATTCA AGAGTGGCTA AG	232

(2) INFORMATION FOR SEQ ID :828:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 282 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25	GGACATTGGA ACACTATACT CTATTATTGC GGCGTGCCT AGCAGTCTCG	50
	CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT	100
30	TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC	150
	TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT	200
	CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTCATCA	250
35	GTAATTACCC CATATCATAA AATGCGGGCG GG	282

(2) INFORMATION FOR SEQ ID :829:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 230 base pairs
	(B) TYPE: nucleic acid

417

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

	CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC	50
10	TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
	AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCCTTC AACGTGCTCA	150
	AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC	200
15	TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 226 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30	TTCCGCAAAT AAAAGAATTG ACTAAGGTAC CAAAACAGAA AATATAACAGA	50
	GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAAG AGATAAAATG	100
	GAAGAGAAAT GCTGTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35	TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTAAAAA TTACAAACACT	200
	CCTGAAGACG CAGACACACC TAACAA	226

40 (2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTCCTT CTTTCTACA GCCTGCAGTT CATTAAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247

20 (2) INFORMATION FOR SEQ ID :832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

(2) INFORMATION FOR SEQ ID :833:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid

419

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

	AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA	50
10	ATGTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG	100
	CCTGAGTGCT TGTGCCACC ACACAACAGA TGCGCCCTTC CTCTTCAGTG	150
	GCCCCCTCGGC TGCTGCTGGG TCC	173

15

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 288 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

	TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCTT ATGACACAAT	50
30	TCCATCATTC TTGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTT	100
	CAGACTTATC TTATATTTTC ACTTCCCCAT ACCTGGAATC AATCACTTCT	150
	CCGAGGGATGC TTGATTCTT TTAGTGAAGA ACAGTCTTG GAAACCAACC	200
35	GTCTAGGGAC ATCAACTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG	250
	AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT	288

40 (2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAAACCAG CAAGTTTTA	150
15	TTAGTGATTT TAAAAGGGGA GGGAGTGTAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTTCACAAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

(2) INFORMATION FOR SEQ ID :836:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 177 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
30	(D) TOPOLOGY: linear

35	(xi) SEQUENCE DESCRIPTION: SEQ ID :836:	
	TCAGTGGAGG AATTAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTAA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

(2) INFORMATION FOR SEQ ID :837:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC

50

15

CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA

100

TGTTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT

135

(2) INFORMATION FOR SEQ ID :838:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :838:

TCAGTGGAGG AATTAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT

50

GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACAA

100

35

GAGGTAATCA AAAACTCGAG CATGTATTC AGGATCCATG ATTGAATTAA

150

CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA

200

40

201

(2) INFORMATION FOR SEQ ID :839:

422

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10

TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA

50

GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCCTGAGA

100

15

TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT

150

CTGAGATGTA CACGAACGAG ATCTTTGAG A

181

(2) INFORMATION FOR SEQ ID :840:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG

50

TTTTAGTGAA CATTCAAGAGG AGTTTGGAAAG AAAGTCGCTG CACAATCTTC

100

35

ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA

150

TGTGAGTAGA AATGGCAGGA GAACTAGACT TCGAAGTAGG AGCTGGAAGA

200

TAATAACATG GGTTAAAAAA AC

222

40

(2) INFORMATION FOR SEQ ID :841:

423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10 CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCCTTGCT CTTGCTGCGG 50
CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC 100
15 GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCCTGCT CACAACCTCCC 150
TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTGC 200
TCTTACTTTT ATGCCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250
20 GTCATTGTTT TGGAACTTCT CCTTCAGCTT GGTCTTTGC CGG 293

(2) INFORMATION FOR SEQ ID :842:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35 ATGAGGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50
TGGGATAGGT GTCTCATTAA AATCTCATAA TCATTTTTT TGGCAGGTCA 100
40 GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCAAA GACACACAGG 150
AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

424

TTTTCTCTCC TTGCCACACA GCTTAGTTT GAAAAAAA

239

(2) INFORMATION FOR SEQ ID :843:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15	TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTC	50
	AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA	100
	CTCACTCACT CTATAATAAA ATGTTGCAC TCAATTATA TAGTAGTGT	150
20	TGTC	154

(2) INFORMATION FOR SEQ ID :844:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35	GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG	50
	CCAGGAGTTG CGTGGAGACT GAGTGGGTT TGTGTGGGTG AGGGGGCATC	100
	TACTCCTCTT GCAACAAAGCC AGAAAGTAGAA CAGCCTAAGG AAAAGTGACC	150
40	TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCTCAGC CTACCCATAC	200

425

	CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCACTAG CAGGTTCCCC	250
	ATCTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG	300
5	ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG	350
	GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT	392

(2) INFORMATION FOR SEQ ID :845:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 200 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20	CAAAGAATAA ATAATTTTC TATTCTGAA AGTTAACTAA TTATTTATTA	50
	GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTTGAGA AAGTGATATG	100
25	AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTCCCTT	150
	GAGCTAATCC TTTATTTATT TATTTTTTC CTTGAGACAA TGTCTTGCCA	200

(2) INFORMATION FOR SEQ ID :846:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 311 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40	TTAAAAAATAC TCTGGAAAGA GCACCTCCAT CGTCATTAA CATCATATTA	50
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426

	GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG	100
	AGGAGCGAGA TCTCCCCAAG CCTCCAGGAT TGCAGTCTGT TTGTGCCTT	150
5	CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC	200
	AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC	250
	ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA	300
10	GAGGAGGTGG T	311

(2) INFORMATION FOR SEQ ID :847:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 287 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25	CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA	50
	CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTGCC	100
	GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC	150
30	CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG	200
	GCAGCTCGAG GCCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG	250
35	CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT	287

(2) INFORMATION FOR SEQ ID :848:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

	GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC	50
10	TCATCCATAC GTTTCATAG CAAGAAAGCT TATTCTCCC AACTACCGAA	100
	TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATT ACCTATCGAG	150
	AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AAACTATACA	200
15	AACACGCAAA CAGAGTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG	250
	AGGCATATNA CCA	263

20 (2) INFORMATION FOR SEQ ID :849:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 279 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :849:

30	TTGTCAGTCA GAATAGGATG TAAAAGACTA TTTCAAAGAG TTAAATTATT	50
	TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG	100
35	CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT	150
	TGACATTAAA AACGAATGGA TACCCAACTC TGAATTCCAT ATCGTTTTT	200
	AATATCAAAA ACACAATTAA AACTACTGAT AAACCAGGCA ACCACCGCAA	250
40	GTTTATCGAA ATCCTGCCGC TACTAAACA	279

428

(2) INFORMATION FOR SEQ ID :850:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :850:

	GCTGAAAGTT	GAAGTGGAGA	GCTTGAAACG	AGAACTCCAG	GACAAGAAC	50
15	AGCATCTGGA	TAAAACATGG	GCTGATGTGG	AGAATCTAAA	CAGTCAGAAT	100
	GAAGCTGAGC	TCCGACGCCA	GTTCGAGGAG	CGACAGCAGG	AGACGGAGCA	150
	TGTTTATGAG	CTCTCGACAG	AAT			173

20

(2) INFORMATION FOR SEQ ID :851:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :851:

	TCGAGAAAGT	TTCAATGTGA	TTAGATTAAA	ATTAAAAGAA	TCCATAAAAA	50
35	TGGAACAAAG	AAGAAGAGGA	ATGAAATTAC	TTTACTTTA	AACAGCATTG	100
	TTATCACATA	AAACACGTAT	CTTACAAATT	CATGGGATAG	CCCATAAATG	150
	GGACTACAGC	AACAATGGTA	GGAGAGTCCA	TCCTTCTTCA	AAAGCAACCC	200
40	AGCAGGAATT	TTCTGTTAAA	AATATTTTG	CCGTAATACT		240

429

(2) INFORMATION FOR SEQ ID :852:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :852:

	ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAATGTTA	50
15	AAGGAATTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACAACATCT	100
	GCTTATTATG AAAGTGTGTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC	150
20	CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAAACG CTTCTGCTTA	200
	TTCCTCTTAT AAAACAAGGG CAATTTGTG AGAGCTACTG ACGATTTCC	250
	CCTCGAAATT TACTATTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG	300
25	TCCTTGCCGT CACT	314

(2) INFORMATION FOR SEQ ID :853:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :853:

	TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTAATTT ATAGATAGCA	50
40	CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT	100

430

ATTTCTTCAG	TGACAAGCAA	ACTATCCCCC	CACATGCCTT	TAATGGCCAG	150	
TGTTTTCGAT	TTGTATACCA	ATAAGCAATC	TAGGTAGAGG	TAATCATATA	200	
5	CTGATACGCT	AACCTTGAA	ACATAATTTC	CAATCTAGTA	AGCTAAAATC	250
	CGGCCAATAC	TGCTTAA			267	

(2) INFORMATION FOR SEQ ID :854:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC	TTTCTTTTTT	TCCAAAGGAA	ATTCATATA	GAGTCCATT	50	
ATAGGAAACA	GATAAAATGT	GAACGGCTGC	AACTGAGATG	GGGGAGAGTG	100	
25	GCTTGGAGCC	CCCAGCCTCT	TTGCTTCTC	TTATCCCTAT	AGGATGGCCA	150
	TTAGGTGAAG	CAGTTTAGCT	TGTTGGTTCA	GACCTG	186	

(2) INFORMATION FOR SEQ ID :855:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGAAAA	GAAACCTACA	AAAATTGTAT	TTCCATATTT	CATAGTCAGC	50
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431

	CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG	100
	GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT	150
5	GGCCCCAAAAA TT	162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 286 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

	TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA	50
20	GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT	100
	GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG	150
25	GAACAAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC	200
	AACATAACAA ACCCAATCGC CCTGTTAATC TTAAATCTTC AACTCGAGAA	250
	AAAGGCTCAT GACTACTTCT AACCATGCCA AAACCC	286

30

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 280 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

	AACTATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACCTTAC	50
	GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTT	100
5	CCCCCTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG	150
	ATTTTTCTTT TTTATAAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC	200
	TTTTAGAAAT GCATATAAAAT GCTCTACGCT CCTTTTTCT GTTACTTAAT	250
10	CGGCGCCAAG GCCTTTACAT GAATACTCAG	280

(2) INFORMATION FOR SEQ ID :858:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25	CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG	50
	GCCAGGCTGG TCTTGAACTC CCAGCCAACC TCAAAGTGCT GGGATTACAG	100
	CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC	150
30	CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTACAT	200
	CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT	250
35	TATACAGGGC TTGAACGTTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG	300
	AGGCAGTAAC	310

(2) INFORMATION FOR SEQ ID :859:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs

433

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

10	TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG	50
	CCACAGCAGG GCCCTCTCAG GCTGGAAAC TTCTGCCAGA GCTGGCGAGT	100
	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
15	AGGAAGAG	158

(2) INFORMATION FOR SEQ ID :860:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 263 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

30	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
	CCAGGAAGGC ACTAATCAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
	TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTCA AACGTTATAC	150
35	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACCTGAA AATAAATCCC AACCCACGTAA CTTACTAAAG	250
	GAATAATGAG CCA	263

40

(2) INFORMATION FOR SEQ ID :861:

434

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10	ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG	50
	GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAAATG ATAAAAGATT	100
15	ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTGTTT	150
	TGATCCCATA GGTCAATTGT TATTACTCTT CTTCAACAGA GTGATTTCT	200
	ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTCA	250
20	AAAG	254

(2) INFORMATION FOR SEQ ID :862:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 37 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35	GTTCCCTCCTT TGTAAATTAT GAAATATTAA TAGTTAGAC TGAGTAATAT	50
	GACATGAAAC AACAAACCTG CACATTCTA ATTTATAACA AATCCGTTTC	100
	CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGTCTGC	150
40	TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA	200

435

10	TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCA	250
	TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT	300
5	TCACCTACAC GTGGCTCGCT TTAGTTGCT GAGCAGC	337

(2) INFORMATION FOR SEQ ID :863:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

20	TGGTGGGTTTC GAGCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC	50
	GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCAGGAGG CCCTGCAAGC	100
	TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA	150
25	ACTTACAATG CCACCGCGA	169

(2) INFORMATION FOR SEQ ID :864:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

40	ATTAAGGTAA AGGAAGACTT TCCATTGTTA AGTAGAAAGA GTGTCCTGCT	50
	ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA	100

436

	CCCTGTTAAA AACAAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG	150
	CGGATAGCAT TATCTTCCTG TGTTCCAGAC TGGAATGAAT TTATGAACAA	200
5	GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGTT TTCGTTTTG	250
	CATTTCTTAC TTCGCAGTAT TTCTCCGCC AAGAGC	286

(2) INFORMATION FOR SEQ ID :865:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 272 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20	ATATAGTCGG CTAGGGATAG TGAAAATTT GGGGCTTGGT TTAGATTGGA	50
	GAGGTATATG GTGGGGTGTGTC TTATAAGGCT TAACTTTGGG AGGGCCAGG	100
25	GCCTTGATTT CTGTCCCCCT TGCCTTGCCTT GGCCTTGAA TTGAAAGCTT	150
	TGAATTAGGC CTTCATAGAT TTTAGTGTGC ATACAAATAA CACGATCTTT	200
	TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTC	250
30	GCATTTCTGA TCTATAAGGT GA	272

(2) INFORMATION FOR SEQ ID :866:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 296 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAAACG GAACGCAAAT 50
5 AAAAGGAATG AGCACGGTTA CAAACTCACA GGATGAGTCC CTGGGATCTG 100
GGGCAGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150
10 CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200
TTTCTAACAC TACAACGCTA ACTTTGGAA CGTATCTACT TCTAGCATGT 250
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG 296

15 (2) INFORMATION FOR SEQ ID :867:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50
30 CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100
CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT 150
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200
35 GTCACCAGGA TGGAAGAAC CTTATAAGCC CCTATCTATC A 241

(2) INFORMATION FOR SEQ ID :868:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC	50
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT	100
10 CAAAGCCCAA TATAACCAAG GGGAAAGGAAT	130

(2) INFORMATION FOR SEQ ID :869:

15 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 310 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

25 TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTTGAAAAA	50
CTAATGAGAA TGGCATAAAC AACATTAAAG CAATATATTT TGAAATTAA	100
30 TTCAAATGGT CAAATTCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT	150
TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA	200
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGAAATT	250
35 TCCCAAGCAC TTAAACAATA AACAAATGCC TCTTTATACA AACCTTCCC	300
AGTAATAGAA	310

(2) INFORMATION FOR SEQ ID :870:

40

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 192 base pairs	

439

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :870:

10	AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA	50
	TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC	100
	CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG	150
15	CAAGTGATGG ATTTAAGGCA AATCTGTTT TTAAGGAGAT TG	192

(2) INFORMATION FOR SEQ ID :871:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 250 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :871:

30	ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG	50
	AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT	100
	TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA	150
35	CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA	200
	TCTATCCGAT GAGATTATA TNTAAACAAAC TCAACTCCTG TCGAAACAAA	250

(2) INFORMATION FOR SEQ ID :872:

40

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs	

440

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :872:

	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
10	AGGATTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

(2) INFORMATION FOR SEQ ID :873:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 270 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCCATAC AATGACAAAC CCCGAACAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAAACT	250
ATCCAGCGTT AGCACAAATG	270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTT ATCTCCAAAG CCAGCCATGG TGTATTCTC	50
20 TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT	100
GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT	150
TAATGACAGC TGATTATTTC CATCTGCAA CTTACTCAAG AATGCAATCC	200
25 AGACTAACAC GACAATAGGA CATCAAGCT	229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

40 TTTGAACTTT CAGCCGAATA CATCTTTTC CAAAGGAGTG AATTCAAGGCC	50
CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTCT	100

442

	TGGTCTTGAC CAGCCTCTCT CATGCTTTG GCCAGACAGA CATGTCGAGG	150
	AAGGCTTTG TGTTCCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA	200
5	AGCACCGTTA ACGAACGCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT	250
	ACACGGAACT GTCCTCGACC CGTGGGTAAC AGTATTTCT GCGT	294

(2) INFORMATION FOR SEQ ID :876:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :876:

	ATTTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG	50
	TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT	100
25	CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT	150
	ACGCCAACAA AAACCGTTAT TAA	173

30 (2) INFORMATION FOR SEQ ID :877:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :877:

	TAATCAAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAATGT	50
--	--	----

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG	100
AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTCG AAC	143

5 (2) INFORMATION FOR SEQ ID :878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTCAAG TGGTTCTGC TGTGGGACTT	50
20 GCGTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC	100
AGTGCTTCCT AATGCCCCA AGCCAGGAGT AAACCCCTGGA ATGAGGCCA	150
GGGCTTCTAT TGCTAATGCC TGTAAACCTT GCTGAATCTA TAACAGAGTC	200
25 TATACCGCTC TCG	213

(2) INFORMATION FOR SEQ ID :879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTAA	50
40 ACGAGATAGA CACATGCTTA TTCAAACAC AGATATGATC CAGTTAATTC	100

444

	CCTTCTTAGA ATGTGCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT	150
	AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC	200
5	TACCAAGAGTA ACCGTCATCC CCTTGAG	227

(2) INFORMATION FOR SEQ ID :880:

	(i) SEQUENCE CHARACTERISTICS:
10	(A) LENGTH: 221 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

	ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG	50
20	AAGCCTCAGG AATTCCATTG CTTACTTTA GTTGTACTT CAAAAGTACT	100
	TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA	150
25	TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTCTAGG AAAAGGAAAA	200
	ATAATCACTC TTTACAAGGT A	221

(2) INFORMATION FOR SEQ ID :881:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 310 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

	AATTGTGGTA TATTCATTT AAAATCGATC AAAGACAGCA ACATACATTA	50
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445

	ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT	100
	CATATTAAAA CAATGATAAG TAATACTTAG AAACTGCATC CTAGAGACAC	150
5	ATCATTGCA TTTTAGAAA AACAGAAACA TATTAGTGTG AAAAGATGTT	200
	AAAAAAATGAA TATTAACCG TCGAGCACAA CACACTACGC CGATAACAAT	250
	ACACCCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT	300
10	GGCGATCCGA	310

(2) INFORMATION FOR SEQ ID :882:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 177 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25	GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT	50
	GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA	100
	CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA	150
30	CGAACTACAA ACGTAACAGC AGCAGGC	177

(2) INFORMATION FOR SEQ ID :883:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

5 CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCTCTGA AGATACACGT 50
ATAAACCGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

25 CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50
GACCTATTTC AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

	CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT	50
	TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TAAACTAGAA	100
5	TTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT	150
	GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTAA CAAATATATA	200
	TATTAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A	241
10		

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 190 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20
(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

	GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAACTCG ACAAGTAACA	50
25	ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA	100
	ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG	150
	CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAAACA	190

30
(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 168 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40
(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

	CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA	50
	CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA	100
5	CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA	150
	CTATAATATT ATACTCTC	168

(2) INFORMATION FOR SEQ ID :888:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20	ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT	50
	GCCGATCTCG CAACCGGTTC CAGTTAGACA GAACATTGTG ATATTCAAAC	100
25	CACTTTCTCG TAATTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT	150
	AATCATATTC TAGTCCACTG TAGC	174

(2) INFORMATION FOR SEQ ID :889:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40	ACACCAACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA	50
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449

	TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA	100
	TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT	150
5	ATATGTGTGT GTACAATATA TAAAAAAATTA TATGGGAGAA AAGAAAGGCA	200
	AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTG TGTGTAACAA	250
	AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT	300
10	ATATATATAT CTGTATATAC AGGTATA	327

(2) INFORMATION FOR SEQ ID :890:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25	TTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC	50
	GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC	100
	TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT	150
30	ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T	181

(2) INFORMATION FOR SEQ ID :891:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 207 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCCTCAC 50
5 TCTCAGGGGA GGGAGGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAAGGAT 100
TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTT GGCAACCAA 150
10 TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG 200
CAAAGAA 207

(2) INFORMATION FOR SEQ ID :892:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25 CTATCACTTC AGGGAAACAA ACAACTAACAA GCCATCAATT CAGAGGGAAG 50
TGATTTACA GTAGAGTGAA CGAAACTTGG GAAGGAAAAC ATCCAAGAGG 100
30 CGTCTGTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT 150
TCTACTAGGA CCACGGAAA CAAAGCAGAT TAAAACACTC TCTACTCT 198

(2) INFORMATION FOR SEQ ID :893:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAA AAATGGGCC CAATACTTT 50
5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

(2) INFORMATION FOR SEQ ID :894:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

20 AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50
ATGGAAACAG CATAATACTA CATACTATCG CGCGGGTTG TCGGCGTGGT 100
GGCGTGCCT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150
25 GAGTGAGCGT GGGAGGGTGT GGTGGTGGA GGTGTGTGGA GAGGTGAGTG 200
TCCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCCGC AAGAGGGAG 250
GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAC 300
30 AATAACCACT ACTCACATAG AATAT 325

(2) INFORMATION FOR SEQ ID :895:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

	ATAGTTGTAC ATTTTTATGG GGTGCATGTG ATATTTGAT ATGTGCATAC	50
5	AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA	100
	TTTATCATT ATTGTGTTG GAAACATTCA AACCTTTCT TCTAGCTATT	150
10	TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTTGTGAAT	200
	AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTGAT ATACTGATT	250
	TCTTTCTTTT GTTATA	266

15 (2) INFORMATION FOR SEQ ID :896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

	AAGAAGAGTC TTCTGCACAA ACAAAACCAT AGTGTGACA AATAGTCATG	50
	GCCAATGGCA ATCTGATGGT CCAGCGGCC CCGGATGACT CCTCTGCAAG	100
30	GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAACT	150
	AGCAGGCCCA GAAGACCGCC CCGCCCCCCTA TGCCCTGGCG CAGGGCC	197

35 (2) INFORMATION FOR SEQ ID :897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

453

(xi) SEQUENCE DESCRIPTION: SEQ ID :897:

	GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT	50
5	GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA	100
	TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTTGCAG GCACAAACAC	150
10	ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT	192

(2) INFORMATION FOR SEQ ID :898:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 224 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :898:

	TGGATGTTT CATTGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC	50
25	TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG	100
	AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTT	150
30	ACATTAGAAC TGACACTGAA AACATAGCTC TTTTCAGTC CACCCCTGGTT	200
	GCTCTAGTAG CCCACAGCCC AATC	224

(2) INFORMATION FOR SEQ ID :899:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 362 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

454

(xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATT	CTCAGAGTT	AGAGAATAGG	ATGGGGAAAA	TTATATTTAG	50
5	TGAGTTATAA	CCAGAATTAC	ATAAGACAGA	TATGGAAATT	TTATAAACAA	100
	AATGCAAAAT	ATTCTAATGT	TTCAATGTTC	TACATGAACA	TATAGGGAAG	150
	CATAGACAAT	AGCCAAAAAT	ATGTTCTGCA	TTCATATACT	AGTTCAAGTC	200
10	CGAGTCTGGC	TACTTCTAG	GTAGTGTGCT	TTTGTCAAA	TTATAAAGAT	250
	ATATTCCCTT	TGTTTTTGA	AAACGAGTGA	GATGCTTAAA	TAGAGTACAA	300
15	TTATCTCATT	CAAAATGTAT	GTTGTTTCCT	CTCGAGAATT	GTGAAGGTTC	350
	TGAGATTTGA	TT				362

(2) INFORMATION FOR SEQ ID :900:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 310 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30	GTATGTAGCC	CAGTGGGTGT	CTTCCCACAG	GGTAGGTACT	CAGTTGCTC	50
	TGGAGGGTGA	CTCATACCTA	AACAAGTGCA	CATCTCCTTT	CTCAGTAAAG	100
35	CCAAAGCAGG	TTTCTACATT	TGGAACAAAA	GAGATCCTGA	CCAGAGAGCT	150
	ATCACTGGTG	GTCCACTTGG	GCCCTCCTTG	ATGGGTGTGT	TCACTTAGAA	200
	AACCAAATTA	CAGATCTGAA	GGCTGCTGGG	TAGGGACAGG	ATTAGAACAA	250
40	AGGGAATGAG	ATTGAATGTT	ATTTAAGGGA	TATTTCTGTC	AAGTTTGGT	300

455

TTCTCGATGA

310

(2) INFORMATION FOR SEQ ID :901:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTG CCTGGCTGAC TACCTGCATA 50
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA 100
GGGGCGGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTGGCCC 150
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

(2) INFORMATION FOR SEQ ID :902:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50
TCAAACAACT AAACTAATCC GATGTTGAT GAAAATTAAA CTGCTACTCA 100
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTACTT TTTAGACTAC 200

456

	AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAACTCCTG TAAAGAGTAA	250
	GAATATGGAA AGGATGAAGC CTCATTCAATT CGGGCATATT AAAAAGAAAT	300
5	TGCCTTCAGA AACACTTGC CTTTTAATAT GTGTAGCTAC AGTAAGTACC	350
	AATGGGCTAA CTAATTGAAG CTAACATTTT A	381

(2) INFORMATION FOR SEQ ID :903:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

	CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAAACGT ACATATGTAT	50
	ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATA GTCCAT GAATAATAGC	100
25	CTCTGCGCTG TTGCGGGTCC TGCAGGAAGTC CTCGGAGCGG CCGTCGCGGA	150
	AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC	200
	ACTTTTTTTT TATCGGCACC AGGCCCGTC CTCCTCCTCC	240

30

(2) INFORMATION FOR SEQ ID :904:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

	CCCTGGGCAG GCTGCTGGTG GTCTACCCCTC GGACCCAGAG GTTCTTGAG	50
	TCCTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCTTAAGG	100
5	TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCCTTAGT GATGGCCTGG	150
	CTCACCTGGA CAACCTCGAA GGGCACCTT GCCACACTGA GTGAGCTGCA	200
	CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG	250
10	TGCTGGTCTG TGTGCTGGCC CATCACTTTG	280

(2) INFORMATION FOR SEQ ID :905:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25	GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT	50
	AAAAAAAAAAA ATAATAATTAA ATACCGTTGG TTTCTACATA CACTCTCAAT	100
	ATTTGCACGA GTAAAGCGTA GCAAGTTAA CACAACTTAT GTAAACTTGG	150
30	AAAATTTCC GAAATTTAT TGACTTTCT CGGTCTCTCC TATCTTTATA	200
	TACACATCTC TCATGCACAC ACGCG	225

35 (2) INFORMATION FOR SEQ ID :906:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 161 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

5. GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA 50
ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA 100
TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG 150
10 TCCACTGTAG C 161

(2) INFORMATION FOR SEQ ID :907:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

25 AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTAAAAAT 50
ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT 100
TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT 150
30 TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC 200
TCTA 204

(2) INFORMATION FOR SEQ ID :908:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

459

(xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
	ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAAGC CTGAAGAAGA	200
10	CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCCTT CCACCATATC	300
15	CAAATGTGTG TGTTT	316

(2) INFORMATION FOR SEQ ID :909:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 307 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :909:

	CTAGTAACAT AGAAAATAAA CTTCAGTGGG AATCTCTGCT TCCCGCGTGA	50
30	GGTGTAAAT TCTTGGCATT TTTGTATTT AAAGATGTAG CAACTTGT	100
	CAAGTTAGAG GAGATGGCAG GGTCAAATT TTAGAAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAAC TG CATACTCAG TATCTCCACG	250
	GGAAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTAA	300
40	GCTATTT	307

460

(2) INFORMATION FOR SEQ ID :910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT	TTTCCAGGCA	CCTAACGATT	TGTTTGCTC	AATCAAACGC	50	
15	AGACAGGGCGT	CTCCGAAGTA	CCACCACTGG	GATATCCTCG	GACCAGCGCT	100
	TAAACCGAAT	CCCCACAATC	TCAAACTCAA	CCAGGCCAAA	GGGAACACAG	150
	TGACACAAACA	ACAGGGTTCC	AA			172

20

(2) INFORMATION FOR SEQ ID :911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG	ATATATACAC	AGAGAGGACA	TACATATATA	TATATAGAGA	50	
35	CACAGAGACA	GACATATAGA	GATATATATA	TACACAGCAT	AGAGATACAG	100
	AGAGATAGAG	AGAGATACAC	ATACACACAT	TCATCAACGA	GAGAGAAGAG	150
	AGGAAAGAGA	GAGAGAGCGA	GCACACACAG	AGATAGAGCA	CACAGAGAGA	200
40	TCGCGCAGAT	CTATACAGAG	GGATATTCAC	CACATTGTAT	ATGGAAAGCG	250

461

CATCT

255

(2) INFORMATION FOR SEQ ID :912:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15	CAAGCGAATG GTAATTACAT GGTCGGATGA CGTCCTCACT CTCAGGGAG	50
	GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT	100
	GAAGCATCTA ACGAAGGGCA ACAGTTTTG GCAACCCAAT TCACAGTTT	150
20	GCAATTTACA AGAGATTCT TTGAAAGAAA ATAGGAAGGC AAAGAA	196

(2) INFORMATION FOR SEQ ID :913:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35	ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA	50
	GCGATTTAC AGTAGAGTGA ACGAAACTNG AGAAGGAAAA CATCCAAGAG	100
	GCATCTGTTT GACGGGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA	150
40	TCCCACCTAGG GCCACGAGAA ACAAAGCAAA TTAAAACATT ATCCACTACA	200

462

CGA

203

(2) INFORMATION FOR SEQ ID :914:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15	CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA	50
	GGGTCCCTCTT TTCCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT	100
	AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTG AAAATAAATC	150
20	TTAGTGTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAATCGGA	200
	TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTT GTAGTATCTG	250
25	GAGGTGGACA TT	262

(2) INFORMATION FOR SEQ ID :915:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :915:

40	TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTGATCG CACCACTGAT	50
	ACACGGAGTC TGTATTTGC ATCCTAGAAT GATTAACCAAG AAACAAAGAA	100

463

AGGAAAAAGG TAAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150

AAAGAATGAA ATAATTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50

TCCAGGAGTT GTCCTTGTT GTTTGTCTG AAGAATTATA CTTTGTGTGT 100

20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150

AGTGTGTGCA TATGTTGTTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT 200

25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250

TG 252

(2) INFORMATION FOR SEQ ID :917:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :917:

40

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

	GTAGGGAAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT	100
	TCCTGAACGT CATCGATCC TTTACCCTCA GAAACTTCA GGCTGAAATC	150
5	ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT	200
	CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC	247

(2) INFORMATION FOR SEQ ID :918:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

	ATTTGGATTC AATTGCCTGT TGCACTTTA CATTAAGTGT TGCTTAAATA	50
	AACAAAAATA GAGCATAAAAT TCAATATTCT ACTGTCTAAA CATTAAAG	100
25	CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT	150
	TGACACCTCT TGTTTAAGT TTCCTGTATG ATAAAGTTCT T	191

(2) INFORMATION FOR SEQ ID :919:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

	CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAAGAA	50
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465

	ACAAACCTCCCT CATTTCAGA AGCGAACACA CCCCCGCCAG AAGATAGACG	100
	ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT	150
5	CGAACAAACAC ACAACCCGCA AAACCATAACA CGCTCCCTTG CCCGAGGCC	200
	AACCC	205

(2) INFORMATION FOR SEQ ID :920:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

	GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCCTC TCCAACCGACT	50
	CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAAGTAATA	100
25	CATCTCCTAT CGTTAGTTGA ATAAATTACAC ACACCGCGTT TAAGAGATGA	150
	AACCACGACT TCGTCAAGGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT	200
	TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA	250
30	AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG	300
	CTCTAAGCTA CAGGTTGATC ATA	323

35

(2) INFORMATION FOR SEQ ID :921:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :921:

	AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA	50
5	GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG	100
	ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG	150
10	GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCAGCGG GGATCAAAAC	200
	TATAGAAACA ACAAGTTAGA GTACAGACGT	230

(2) INFORMATION FOR SEQ ID :922:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 239 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25	TATTTTCCCT GATGTTCTCC CTTCCCTCCAG TCCCCGACCT CCCACAGGCC	50
	CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTAG	100
30	TGCCCATTCCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCCTCGCTC	150
	TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC	200
	TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTTGTAA	239

35	(2) INFORMATION FOR SEQ ID :923:	
	(i) SEQUENCE CHARACTERISTICS:	

40	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5 GTCAGTTCAAG TTGTGAACAA AGCCCTTTGT GTACGTTTT AAATTTAGT 50
 TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT 100
 TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC 150
10 TGAAACCCGT CCACTCAATA AATTTTG 178

(2) INFORMATION FOR SEQ ID :924:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25 CAGCTGGTCC CCCACTAAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG 50
 ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCC ACTGATTCCC 100
 AAAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTAT 150
30 TCTTGCTTCT TGTTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA 200
 GCAATCTCAT GGTTCTTGGGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA 250
35 GTAATCAGAG AGAAAGATAAC CAAGGAATGC TTTTCTGGC CTATTCATTT
 ATTTTTGGGG GATGAATTAA CAGTA 325

(2) INFORMATION FOR SEQ ID :925:

40

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

	ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG	50
10	AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT	100
	CCGGTTTTCT TTGTTTTTC TCTTTATTCTG TCCTTTCTCA AAGATGGGAT	150
15	ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG	200
	AAGCAGCTGT GGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG	250
	TTCCAGTCCT G	261

20

(2) INFORMATION FOR SEQ ID :926:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

	GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC	50
35	AACTGGGTTTC AAATCCTGGC TCTGTCACAT ACTAGCTGTG TGACCTTGGC	100
	CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGAT	150
	AACCAACCAA GAGAGCTGAG AGA	173

40

(2) INFORMATION FOR SEQ ID :927:

469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC	50
CTCGCTTGCT TTGTAGTTT CCCGCACCAAG CCCGCTGCCG TGCGCCATCC	100
TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC	150
CTTNGATTTC TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC	200
TCAGATCATT ACTACTGAAC TCG	223

20

(2) INFORMATION FOR SEQ ID :928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTAA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT	50
ATTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTT AAGATAAAAA	100
CCACAGATTAA AGTGAAGACA CCCACAACCT TAATGACTCT ACGACTCTCG	150
GTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTCAAG TCCTACCTGT	200
CATAACTTGC AT	212

40

470

(2) INFORMATION FOR SEQ ID :929:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :929:

	TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT	50
15	ATAAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT	100
	TACTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTGTG	150
	TATAATGTTA TGTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG	200
20	ACATAACTTG AGTTGTTTG CTTGGTATTT ATT	233

(2) INFORMATION FOR SEQ ID :930:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35	AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA	50
	GATCAGATGG CATCCAGAAG ATAGTTAGA TTTCAGCACA TTCAATGGTTC	100
	AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTAC AATCATCATA	150
40	GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC	200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

(2) INFORMATION FOR SEQ ID :931:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15

CTATCTAGAA TTACTTATT CACTTGAAAT GTATGGTTTC AGGAAAATTT

50

TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGA ATAATGGCAT

100

20

CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTGGGT GAATGCTTAA

150

AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC

200

ACACACACAC ACAAAAAACA C

221

25

(2) INFORMATION FOR SEQ ID :932:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :932:

40

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG

50

CGTCATGTCT TGTGCTACTA CACCGTGTAA ATCCAGCTA CTCAGGAGGC

100

TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA

150

472

	TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG	200
	GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA	250
5	ACGGAGCAGG TCAAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT	300
	GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA	333

(2) INFORMATION FOR SEQ ID :933:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20	AGATTTATGG CTGCTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAACAA	50
	GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT	100
25	TGTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTCTG AATGTTAAG	150
	AAAAAAATAA TACTTTCAAG AATTACCTAC CTCTTCTCA TTTTTAGCCT	200
	GGGATCAATT ATTCCCTTTC ACACTTTTT ACATCCTAAG TAGAAATAAA	250
30	ACTCTTTATT CTATTTTTT TCAGTTATTG G	281

(2) INFORMATION FOR SEQ ID :934:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

	AATCTTGTAT TATGTTAATA TTAAAATCTA ATAATAAGAT ACTGTAGAAG	50
5	TATTTTACAT TTTTGGGTA TAGGCACAAA TATATACATT TAAATATTAG	100
	TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAAACTGTT	150
	GTTTTATCCC AAGGGTAGAG GGACTCTAAG TAAAACTGTA ACAGAATCAA	200
10	AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTAA CTTGGGAACT	250
	TTAAATAAGT AAATCT	266

15 (2) INFORMATION FOR SEQ ID :935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

	GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAACT	50
	ACTAATAACT CATTAATAAA ATTAATAATA TTAAATGATC TGTGTGTTCC	100
30	ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA	150
	TTACTCTAAC ACCAATAACA ACACGTAA	178

35 (2) INFORMATION FOR SEQ ID :936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :936:

	ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAGAGGC	50
5	TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCT ACAGCAACTT	100
	TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG	150
10	AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC..TGAAAGTTAG	200
	ACTTCACCCG AATTACATTT ACCA	224

(2) INFORMATION FOR SEQ ID :937:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 270 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25	ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACATTGCT	50
	GGGGATGGGT AGAGAAAACC CATTATAGT ACTTTCTGC CTTCTGTGG	100
30	TTTCGGCTT TCGGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAA	150
	AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTCCAA	200
	CCAAAACCTCC TAAAAAACCC AAAAACAGAA CAACCAATTAA AACCCGACCC	250
35	GACACAACTA CCAATGACTG	270

(2) INFORMATION FOR SEQ ID :938:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 215 base pairs	
	(B) TYPE: nucleic acid	

475

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCAATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACCGACAATG GCACCATTGA	150
	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
15	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 303 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCTGCCTT AATATTTCTN AGCCTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTGTC TATGTTCTA TATCTCTCTC	100
	TTTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT	150
35	ACCTTCATGA TTGCTTTTA TTATTTCTT CACTCATCAT TATTGTTCAT	200
	TTTTAAATTA ACAATTTTT TCATTATTCT TTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TGCGCTTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

(2) INFORMATION FOR SEQ ID :940:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :940:

	ACACTATTTT CAAAAATCCA AATAAAAGTG CAGTTTCAGA CTTTTTAAAAA	50
15	AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG	100
	CGTTTGCATG CAACACTGCA TATTTTTCT AATCAGATTA ATATGAGTTT	150
	TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTA AAGTAGCTT	200
20	CATAGTCTAG ATTCCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT	250
	TGCTTTGCTT TGTGGAGACT TGCGCGTATT TTCTTTGCT TGTGGTTA	300
25	TCGCCAGGCA GCGCTGTTCG AACTGTGAGA	330

(2) INFORMATION FOR SEQ ID :941:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :941:

	TTTATTCAG ATAATTTAT GTAAACAAAT TAAGACTTAT TCATTCAAAT	50
40	TTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT	100

477

TTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTGT GTGTGTATGT 50
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT 100
TTCGGCGTTA CACCTCCGGT GTTCTC 126

20

(2) INFORMATION FOR SEQ ID :943:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTAACAGC CGCTGGTTCC AGAACAGGCA CAGAACGGCTC CAGCGCTAGA 50
AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100
GGCTCCGGGA CAGTCACAAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150
AGCTC 155

40

(2) INFORMATION FOR SEQ ID :944:

478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC	AGGTACCATT	TTTAGTAGTC	ACACAATTCC	ACCTCCTGTT	50	
TTTACTACTG	GCAACTTCTA	CTTGAGAATA	ATGTTCTGAA	AATGGAGGTG	100	
15	GGGGGGGGTT	TGGAAGCAAA	CACATTTGGG	GTTTTAACC	AATTGTTAGG	150
	TTCTTTTTAT	TTAGGGTTGT	GCAGGGAACT	GTTGGGAGGT	TTCTTTAGGT	200
	GGGATGGGGG	GACTGGGTGT	TGGTTTTG	GGGTTTTG	GGACGGGTTT	250
20	TATTTTGTCC	CTTAACCTGG	TTTGTGGC	AGGTGGG	287	

(2) INFORMATION FOR SEQ ID :945:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35	ATCATTGATC	AATGATATGG	TTTGGATTAC	TGCCCGGCC	AAATCTTTG	50
	TCCAATTATA	ATCCCCAGCA	TTGGAGGAGG	GGCCCGGTGG	GAGGTGATTG	100
	GATCATGGGC	ATGGACTTCC	CCCTTGCTGT	TTTCGTGATA	ATGAATTCT	149

40

(2) INFORMATION FOR SEQ ID :946:

479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTTAAATA	50
AATTCACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG	100
15 AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTAC	150
ATTAACATTG GAAAACCTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA	200
20 GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAACGGT TTCTCTTTT	250
TTTTTTCCC C	261

(2) INFORMATION FOR SEQ ID :947:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACCTCG	50
CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAAGTTG CACTATTGCA	100
40 AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTT GTACTGCTGG	150
TCCTGTACCA GAAACATTT CTTTATTGT TACTTGCTTT TTACACTTG	200

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC	250
CAAGTTGTAT ATTT	264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTGA	50
GCCAGGTTGA TTGAGCACTG GGCTCCAAT TATTGTTAAT GAGAAACGGC	100
20 CCAAACTTGGA CCATGACTTT CCCATTTGCA GGTCTTAGAA TAATTTTT	149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCAG	50
GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA	100
40 GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG	150
TTCTAGTCCC CTTTTAGAT CCTAGGGGAC TGGAGATTTG GCACCTTCCC	200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15 ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG 50
CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC 100
AAAGTTTATA CATGAAAATT TAAAAAGGGA GTCTATGCAA AGCGGAGTTC 150
20 AGG 153

(2) INFORMATION FOR SEQ ID :951:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35 TGCAGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG 50
TTGTTCTAA GGCGAGCTCA GGGAGGGATAC AGAAAACCTCT CCTGTGGTGC 100
TATGAAATGT GGCGTAAAAA GCATTCTG 128

40

(2) INFORMATION FOR SEQ ID :952:

482

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10

GTGGAAATT TCCCTAAAT CACCTACCGA TTACCCCTTGA TTTCCCTTG	50
TTTCAGTTT CTCAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC	100
ATATAAAAAT AAAGTGTACC CAAATATTGT AATGTATATT GCTGCTCTC	150
TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC	200
AATTGATACA AAT	213

20

(2) INFORMATION FOR SEQ ID :953:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :953:

35

GCAGCAGTTT CTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC	50
TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT	100
TCATTATTT TTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC	150
CACAATCCTG GATACTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT	200
GCCACTGCAG AAAGTGTAGT ATTTCACTA CATTAT	236

40

483

(2) INFORMATION FOR SEQ ID :954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :954:

	GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC	50
15	TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT	100
	TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAAC	150
	CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT	200
20	GCCACTGCAG AAAGTGT	217

(2) INFORMATION FOR SEQ ID :955:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35	AGCAGCGACC GCGCTCACTG GCTTTTGTT TCTGCTTGGG CCTTTCTGT	50
	TCAGTCCATG CTTGAACTAC TCCACCCCT TAAATCCAAC GTAAAAACCA	100
	GTCTTTCTG TGCTTGTCT CTGTGCGTTA ATGCTTTTC TTATGCTTGC	150
40	TTATTGAAAT ACTGTATTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG	200

484

TGAAACCATT TTAGATACTC TACTTCTTA CTGTGTTACG TGGCATTAA

250

TGCTTG

256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTT TTCCTGTTAT TTTCTACCA TTTATTCTC

50

ATTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTATT

100

AATTTTAAA AATAACATTA AAAAATTTT TAAAATGTGA ATATACCACA

150

ATACAGTATA AAGATTGTAC ATTCTGTTT TGGACAGTTT TCTA

194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA

50

ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTAGG GTGAATTCCCT

100

40 CATTTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG

150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

(2) INFORMATION FOR SEQ ID :958:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15 GCGCTCAGCT GGAACCTCCG ATCTATTTT TCTTGGTCTC ATACTCAGTT 50
 TTTTTATGTA GTCACTTAGT AAAATAAACCC TAAAAAAA CATTGATTTT 100
 TTCTG 105

20

(2) INFORMATION FOR SEQ ID :959:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

35 GACAGCGACC GACACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA 50
 GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA 100
 TAATTCAATTA ACACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT 150
 TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC 200
 40 TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG 250

CTTTTGTAA A

261

(2) INFORMATION FOR SEQ ID :960:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15	CACAGTTTG TTGACTAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA	50
	TCGTTTCTTC TTTAGAGGAG TAGGTTTAA CCATGTTAAA TTTCCAAGAA	100
	TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTCA GGAAAATAAA	150
20	TAATTTTCGA TTCAAGTACT ATACAAACTT AACGATGG	188

(2) INFORMATION FOR SEQ ID :961:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35	ACTTTCGCCT ACCCGGAGAG GCCCAGAAA TTGACCAGAT GATGGAGGCC	50
	TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA	100
	CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTAAC ACCAATTCT	150
40	ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C	191

(2) INFORMATION FOR SEQ ID :962:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT 50
15 ATTCACTGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGT 100
TCAATGAATA TACAACGTGAC TGGATTTAA ATATACACAA ACCAGTATA 150
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAAT T 191
20

(2) INFORMATION FOR SEQ ID :963:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCAGC AGGAACAGCA GCCCAATGCC 50
35 TCCTAGCACT CAAGATCCAC CATA GTCCAA GCAACTGCAG TTACACTTGA 100
GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCCT AAAGGACACC 150
CGAACACCAT CAATAACCGA ATAGACTA 178
40

(2) INFORMATION FOR SEQ ID :964:

488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10 ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50
GGGATCCTTT TGACTGCCAG ACGCGGGAAAG GAAAGAATGA AATTAAGGAA 100
15 TATCCTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150
CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

(2) INFORMATION FOR SEQ ID :965:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :965:

30 ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATAACCCAC AGTGTATTT 50
GGCACATCTG CCAAAAGCTA CAAACAAACCC CTAATAATTA CACACTACAG 100
35 ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150
CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTCTCC TCGCCTTAA 200
ACCTGCAGGT TGGGGCT 217

40 (2) INFORMATION FOR SEQ ID :966:

489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTCC	50
AATTTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT	100
15 CAAGAAAAAG CAAATGGTTT AAGTTTTAC ATAGGAAATC TAAGAACTAC	150
TCATCAATAA AACGCAACAC TATCA	175

(2) INFORMATION FOR SEQ ID :967:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTCAAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG	50
GGGGACAAGG AAAACCTGGC GCCCCCCCACC GCGAAAAACA CA	92

35

(2) INFORMATION FOR SEQ ID :968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

490

(xi) SEQUENCE DESCRIPTION: SEQ ID :968:

	GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCA ACATGGAAAA	50
5	TATTGTCAG CAGGAAAGT AAAACTTC AAAAAATTCCC TAAAGATCCT	100
	ATTCAATAAA CAATTTAGA TTTAAGGAAC CACTTACGCA AAACTCGAAC	150
10	AAATAACCGA AAACCTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA	200
	CTACTAAC	208

(2) INFORMATION FOR SEQ ID :969:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25	AGTGGTTGGT GTTTACTGGA ATCTTGTTC TTTTTTTTCG GTTTTTTG	50
	CTACTCGGGG GGTTTTCCTT TTTTACAGGA ACTAAATCAA CAAACTTTT	100
30	CGATTCCCTCA ACTTTAGATT TTTATTTTT TTGATTACCA TTTACTTTTC	150
	TTCATTTAAA ACTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC	200
	CACCAAGGAT TTACTCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT	250
35	TTAAGA	256

(2) INFORMATION FOR SEQ ID :970:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 240 base pairs
	(B) TYPE: nucleic acid

491

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

	AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACCTAGTA	50
10	AATAACCTAA CCCGCTTGT TTTTCCACAC TAATACTAGG GCGAATTCCCT	100
	CATTTTATT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA AACAAATGCCT CTATTCCTTC AAGTATAATA	200
15	AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240

(2) INFORMATION FOR SEQ ID :971:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 184 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30	ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGT TTCTCCACACT AATCCGAGGG TGAATTCCCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGG AATGACCGCG TGCGCGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCCCTC TGCT	184

(2) INFORMATION FOR SEQ ID :972:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 234 base pairs
	(B) TYPE: nucleic acid

492

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

	GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTAA	50
10	TCGAGAATTTC CCAAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTAA	100
	CATAATCCAG TGAAAACCTCT ACTTGTTGAA ATTATGACAT AAAGATCTTG	150
	CAGCTTTATT TGAGTATTG TTCTTTGTG TAGTTCCAT CTTTTAAAAT	200
15	ATTTAAAATA TTTTCAAGGA TAAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 197 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

30	TTTTCATCTA AAGGAGAGAG GCAGGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
	TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	100
	AAAAAAACAT CACAAAACGT AACTGCCGCC ATCACCACCA CACCAAGTAT	150
35	GTGATTGAAT TATTCAATGA TCTGTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 244 base pairs
	(B) TYPE: nucleic acid

493

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

	AGCAGGAGAT TTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGACT TAAAAAAATA	100
	ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC	150
	ATACAGAAAA AAACGAAATA CATAACCCCC CAGGTTGAA AGAAAATAAT	200
15	TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC	244

(2) INFORMATION FOR SEQ ID :975:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 330 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG	100
	AGACCCATTA GAGATTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA	200
	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300
	ATGTGCAATG AAGGGTTTCG TGTAATATTG	330

494

(2) INFORMATION FOR SEQ ID :976:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :976:

	TGGTGAAAGG AATAAGCAAC TCAAGGTTAA TAAAGAAGAA AGATGAAGAT	50
15	TCTTAGAACG GTAGAAAGAC TGCAGGGGAA AATAATTAAA GCAGCTTTAT	100
	TCCTTACGGC ATTCAATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT	150
	AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA	200

20

(2) INFORMATION FOR SEQ ID :977:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :977:

	AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT	50
35	ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT	100
	AATGATGTTA TGAAACGAGC TTTGCT GCTCTTGATT GGAGCTTCCG	150
	GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC AACTGTGTTT	200
40	AATACTCTGA ATTTAATTA GAAAAAAATA CAATAGCAGC AAGGCCCTGG	250

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

(2) INFORMATION FOR SEQ ID :978:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15	GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG	50
	ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT	100
	AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAAGC CGGGGGAGGA	150
20	CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCCAGAATC	200
	CAGCCACTAC TGATAATTCA CAACGGTA	228

25 (2) INFORMATION FOR SEQ ID :979:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :979:

	CGTACAAAAG CGCTTGGAG ATGCCAGAAA AAACCCCTACG GGAGGGTTAT	50
	CCCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA	100
40	AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA	150

496

CCAGGCCAAA CCAGAACCTG A

171

(2) INFORMATION FOR SEQ ID :980:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15	TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC	50
	CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC	100
	CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTT CACACCAATG	150
20	ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTT TAAAGCATT	200
	CTGCAGTGGAAATAACTGC ACTCTCAGGA CACAGCACTG T	241

25 (2) INFORMATION FOR SEQ ID :981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :981:

	TCACTGCAAT CACGGTAGCT TCGCCCATTG CCTCTTCAAC CAGGCACATA	50
	CATCGAGAAG TTGAACCTGC ACTTTATTTC ACAGTGAACA GACTTACCCC	100
40	GACAACAAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCCACACTC	150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AAACATTTGC 200
AAAACCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50
ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100
20 CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA 150
CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200
25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTAA AAAATGATCT 50
40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA	150
CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC	200
5 CCCT	204

(2) INFORMATION FOR SEQ ID :984:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

20 ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTTG CATTCTTGTT	50
TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT	100
AAGTACTGTG ACTTTAGCT GCAAATCTT GCTCTTGCT TTTTTTTTC	150
25 TTTCTCCCCC CTCCCCAG	168

(2) INFORMATION FOR SEQ ID :985:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :985

40 CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAG AGAAGCATGG	50
GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT	100

499

	TTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG	150
	CTGGGAGGGG GGCCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT	200
5	GGTCCAGCCC CTTACGCCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT	250
	CCTGATGTAT TTTTTTTCC TCCAACCTCAA AAGGCAAAAA TAATCCTATT	300
	TTTATTATCT TGCTACAACT GCAACTTCTC GCCCTATAAA TTTACATTCC	350

10

(2) INFORMATION FOR SEQ ID :986:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :986:

	AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAAGGTG AGCCGCTCTT	50
25	CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT	100
	TCAACAATGC TCTGCAAATC TTTTTAAGAC CCGTTACTTC AACAACTCCC	150
	AATAACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA	200
30	CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA	250
	AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAAA	289

35

(2) INFORMATION FOR SEQ ID :987:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

500

(xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CACGATTAC ATCTGATCCT CACGCAATT 50
TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA 100
CATTCTTTA TTCTTGCATC GCTATAAAGA AGTA 134

10 (2) INFORMATION FOR SEQ ID :988:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGACTGTAGG ATTTGTAATT 50
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100
25 ATTCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150
GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200
30 TCATAATTAA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250
ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

35 (2) INFORMATION FOR SEQ ID :989:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

	AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT	50
5	TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG	100
	AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCAAC ATATTTCTC	150
10	CTTTCATAA AGAACCTAT ACACCAT	177

(2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 158 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :990:

	TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA	50
25	TAAACTAACCC ACCAACCAAA GGAGGCACAA TCCAACGAAA	100
	CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAC	150
30	CAAAAGTC	158

(2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 267 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

	TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTAAA	50
	AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTAAT TCATTTGAT	100
5	TACACAAAAAA TAAGGCAAAC TAAATGATTG AGAACAAATTC AATTAACTG	150
	AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAAG ACTTAGCGCA	200
	CATAAAACAA TCACGAAGAT CACAATTCA GCACAAATAT CTGAAGGAAT	250
10	ACACGCAAAA CATCATA	267

(2) INFORMATION FOR SEQ ID :992:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 199 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25	AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA	50
	TTGTCAAATT CCACTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT	100
	CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA	150
30	TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA	199

(2) INFORMATION FOR SEQ ID :993:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

	TTTAAGGTGC TAAACTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG	50
5	ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCAGG	100
	AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT	150
10	AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC	198

(2) INFORMATION FOR SEQ ID :994:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 183 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :994:	
	GCTATCTGCG GGGCCATTG TAGGATGGGT GAGTCAGATG ATTCCATTCT	50
25	CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGACTGGAGA	100
	GAATAACAGA CGTGGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA	150
30	AAAAAAAAAA ACAACAAACC CCAACAAACT CAA	183

(2) INFORMATION FOR SEQ ID :995:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 199 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40	(xi) SEQUENCE DESCRIPTION: SEQ ID :995:
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504

	ACCTCTGCAT TAACACTCCA GCACCTTGG TTAGCCAATT TGGCCTTATT	50
	TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAAGG AATGTTTCG	100
5	GGTTACCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT	150
	TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA	199

(2) INFORMATION FOR SEQ ID :996:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

	GGTCTTGGCT GGTGGTTAT GGGCCGGGCC TTCTTCTAC GGGGGCCAGG	50
	GTCCAATTTT CCACCTGGGG TTTAAAAGTT AAGGAGGACC AGCCTGGAA	100
25	CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTA	150
	AGGGGACACC ATATGGAGAT TTTATGC	177

(2) INFORMATION FOR SEQ ID :997:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

	GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCA	50
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505

	GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTC	100
	AGTGAATAAT TCCTCTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC	150
5	GTAGAAAGTT GCTTGAAATT CTTTCCTAA AAAAATTAA TTTTCTATC	200
	TCAAAATGAC CGTATGCAA CGAACATTA	229

(2) INFORMATION FOR SEQ ID :998:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :998:

	TTGCAGTGT TATGCCGCC TTCTTCACG GGCAGGTTCA ATTCACTGG	50
	TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG	100
25	GTCCCTTAAT TTAAGGAACA AGTTGATTAA TGCTACCTT TTGCACGGTT	150
	TAGGGTACCG CGGCCGTTAA ACATGTGTTTC ACTGGGCCAG GCGGTGCCCTC	200
	TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT	233

30 (2) INFORMATION FOR SEQ ID :999:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

	TCAAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGCGTT	50
	CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA	100
5	TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAAACCACC	150
	AGTGGAAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC	200
	TATCATGATA TTAGTT	216

10

(2) INFORMATION FOR SEQ ID :1000:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 280 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

	GACAAGACCT AGAACCAACA ATGCCAGTA GAAACAAACA CACCTACTGC	50
25	CTGGATCTTA GTTTTAATT ATATTCCCCA ATAAAGAGAC CCAGGGCTCC	100
	TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA	150
	CCTAGAATAT CTAATACTGC CAAAAATTAA GAAAGTGTTC TAAAAAAAAT	200
30	CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC	250
	CCAATGGCCA AAGATCAAAT AATTTTCAA	280

35

(2) INFORMATION FOR SEQ ID :1001:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 324 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
5	CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGGAAAGCTTA	100
	GTCGTTTCAG CCCCCATTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACCA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC TGTTCATTTG TATC	324

(2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 254 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		

(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTTCCATTC ATAAGTCCTC ACAAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCTCCC GCAGAGAGGC ATTCCCTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCCCTCC TCCAGCAAGC TTCTTAATTC	250
40	ATTT	254

(2) INFORMATION FOR SEQ ID :1003:

508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCGC	TGCCCATCCT	CTCGCCCTTC	GGAATTTACC	CCTGGCCGCT	50				
CAGGGTCTCG					CTTCTAGAAG	AAGATGATGG	ATACTAGGGC	GATCCTCCTA	100
15	TTGCCTTAT	ATTTAACAGG	CCCGCCGAGG	AGGGGCTCCC	GCTGGTGCCC	150			
ACATAACTCT					ATTAGACCAT	CTGAGGGCGAC	TTCCCCCACC	CCCTCCAACG	200
CGCCTCACGC					ACGACTCTAG	CAAAAGACAG	GTTCCGCGGT	GGTCACGTCG	250
20	TTTGAGACTA TACTG					265			

(2) INFORMATION FOR SEQ ID :1004:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35

AAATATGCC	TGAGGATTAT	CTGATGTCGA	TGGTGTGGAA	AAGAACTCCA	50					
GCAGGGCGACT					TGATTCAA	TCAATGTCCC	CTGAATGCCA	CAGAACCACT	100	
AGCAGACGCT					GCTCTCTCAG	TCTTAATGGA	GTGGCCTTCT	GGGAACAGCC	150	
40	GAGCTTGAA					AGATGCATAT	CAAATGAGTA	CAGACACTTG	TAGCATTAA	200

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250
CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50
CTTCCATCTC ACTATTCCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100
20 TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA 150
GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTCGAATT 200
25 GTAAAATCGT GAGCCACTCA TATTCAAAC T AAAAAAAGAA CAGAACTTTT 250
ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA 300
CGCTTGCATT CATAAAG 317

30 (2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTCCCT GGAATGCCTT	50
TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCAATCCTT AACAAACCTAG	100
5 CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC	150
TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA	200
TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA	250
10 GAGTCTTGT CTAAATACTC AAAACCTGT TTACCAT	287

(2) INFORMATION FOR SEQ ID :1007:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25 GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA	50
CTGTCTCATC GGGGCACCTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA	100
30 TGCTGTATTC AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG	150
TAAACTTTGA AGCCCTTGA AGGACCTAAC CAAACAAACAC AAGGATGAAA	200
ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA	250
35 TATTCGGATT TTACCGTAAG GAA	273

(2) INFORMATION FOR SEQ ID :1008:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

	TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT	50
	TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC	100
10	CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT	150
	GCGCCCTCTC CCTGCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGCA	200
15	TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG	250
	GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG	300
20	CAAAAAAA	308

(2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 187 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

	GAACCGCCTC TGTTTCCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA	50
35	GCAGTTTGA AAACCTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA	100
	GGGACAAAGTG TTTGGCGGGA ATGTGTGAAG ACCTAACTAA TGAGTGTAC	150
	TGAATCACAC TATTACACAG ATGAAACAAA GCCTTA	187

40 (2) INFORMATION FOR SEQ ID :1010:

512

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG 50
ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA 100
15 AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT 150
AAGCTACTTC TCCTTGATAT TACCT 175

20

(2) INFORMATION FOR SEQ ID :1011:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

TGAAAAATAT TTGGAACCTCT TTAGTACAGA ACAGTTCAA TATGAGTTAA 50
GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA 100
35 CAGAAGCAGA CCAGCTCAGC TGGGAAACGT GATA GTGATA ACTACTCGT 150
ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG 200
TATTTTAT 208

40

(2) INFORMATION FOR SEQ ID :1012:

513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCA GT ATTGAA TGAGGCTTTC TTAGGAGTAT 50
GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCCTCTG 100
15 ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG 150
ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA 184

(2) INFORMATION FOR SEQ ID :1013:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AAACAGTGCT GTTCCCCGGG GAGGAAACAC 50
ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC 100
35 ATACCTTGTT TATCAAATGA GCGACTCAA ATGATTAAA ATAATGCTGT 150
TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC 200
CGGAAAGAAG CATTGAT ACTTACTGC GAGTAAAAA TCAATACGCA 250
40 GAATGGCATT TGA 263

514

(2) INFORMATION FOR SEQ ID :1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

CAAATTAAGT	GCCAGAATGA	TGCAGCCCGC	TCTCACCAGG	AAGAACGACA	50	
15	TGTGAGAAAA	CTTATAGCAG	ATGCAAAAAT	GTCAACCCAC	CATGTTATTT	100
	AAAAAAAAT	ATGACCAGGA	TACAAGGACA	CTTCACCGTT	TTTAACCCAC	150
20	ACAAGGTCAG	GTAATGTTA	CCTTGAAACA	CAATCGCATA	TGACCCTTTA	200
	TGCCACTCAC	CTAGGCCTTT	AATAATGAG			229

(2) INFORMATION FOR SEQ ID :1015:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35	GAAAATAATG	ATTCATATTA	CCGGGTATTT	CTTATCCAGT	CTTCATTCT	50
	ATGTAAATTG	TGTGTGTGTC	TATATATGCG	TGCATGTCTC	TCTCTACATG	100
	TATATGTGCA	TATGTATGTA	TATATATGCA	TATGCACATA	CATGCCACAC	150
40	ATGCACATAT	ACACACACTC	ATAGAGAACCA	AAATTATTCC	GAATATTCA	200

515

TGAGGTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

(2) INFORMATION FOR SEQ ID :1016:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15

TTCATAATCG CTGGCACTGA ACAAAAGTTGC AGAATTCTTT GCCAGGTACT

50

TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC

100

20

AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG

150

ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA

200

GAATTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC

250

25

AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA

287

(2) INFORMATION FOR SEQ ID :1017:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

40

ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA

50

CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTGAA ATGCTGTTG

100

516

	TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG	150
	TTAACCCACAA TCAGTTCTAC ATAATTAAAC AGAAAACATC TGGTGGCACT	200
5	TTTAAATGTT TAAGGACAGC ATTTCACAAA CTAAGCCCGC CCCCAGTCCC	250
	ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA	299

(2) INFORMATION FOR SEQ ID :1018:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20

	ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT	50
	GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT	100
25	TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG	150
	TGGGTTTGAG GTGGGCCAA GAATTTCCCT TTTAACAAAG TTCCCAGAAG	200
	ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTC	250
30	AAGAGGACAA TCTAAAGTGC TCCC	274

(2) INFORMATION FOR SEQ ID :1019:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

	TTTCTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAAA	50
5	CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
	CATCTTCTAC CACTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
10	AAATGGCACC TCATCTTGA TCAAAGATTC AG	232

(2) INFORMATION FOR SEQ ID :1020:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 133 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25	AACAGTCCAT GCTGATCTTA GTAACTATGA TGAAGATGGT GCTTGGCCTG	50
	TTCTTCTTGA TGAATTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG	100
	CAAGAACTAT GTGAAGAAAA TGCACACCTT TAC	133

30

(2) INFORMATION FOR SEQ ID :1021:

	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 280 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

	TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT	0
	ATTTAAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG	100
5	ACTGTTGAAA GTTTAAGTAT TAGTAAACTT GAGTTACTTT TTCTTCAAA	150
	TTTCACTCCG CTTCCCTGCA TTTCGAAGCT GCTCTTCTG GTCCTACCCA	200
	CCACCCCCACC AACAAAGACTT GTGTTGTTA ATAGAAATAA TTTATCAAGG	250
10	TATTGGGGAT CCATTGTCTA TATTAAAAC	280

(2) INFORMATION FOR SEQ ID :1022:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25	AAAATAAAATA ACTTCTTAGA TTTTGACTG AAAAGATCTG AGAATGTTCT	50
	GCCAAACAGC CGACCAACTG GTGCAAAAGG TTAAGGCTGA CTTGACTTAG	100
	CAACCTGCAG CACAACCAAA AACACTGATG CAGTCAGAG CTCTCAAAT	150
30	GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA	200
	ATCCTCTAGA CAGTTTCTT TTTGTTTGC ATGCATCCCG TTCCATTTC	250
35	ATTACGGGCA TCTATTCCCTT GATCAATTAT GTGCTTGCT TTTTAATCGG	300
	TTTT	304

(2) INFORMATION FOR SEQ ID :1023:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs

519

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

10	TTTCTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA	50
	CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
15	CATCTTCTAC CACTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
	AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT	237

(2) INFORMATION FOR SEQ ID :1024:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

30

	GGCATGATTA TTAGAAACTA TTTAAGCTTT TTTCTTTGAA AAACAAGCTC	50
	CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC	100
35	TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT	150
	TTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAAATAG ATAAAAGTGG	200
	TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT	250
40	TTCACTTGTT TAGTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT	300

520

TAGAGCCAAC AGGAATCTGC

320

(2) INFORMATION FOR SEQ ID :1025:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15 TTCTGGCACC ACATTCAATA CTGATTACA GGGATCTAAA ACATTCTAGT 50
TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA 100
ATATTTGAGG ACTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG 150
20 TTCCACAAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT 200
CT 202

25 (2) INFORMATION FOR SEQ ID :1026:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

ATTGGTAGAC AATATCATAA GAGTTTCTG ATAAAAGATG CTTTTAACCC 50
CTGACTCCCCA GTCACAAATTG TGGCATCTCA TCCATGGGAA AAAAATAGGA 100
40 AACTTATACA TTTCATAAAC TAAAGGTCAT CCAAAACACTG CCAAAACGT 150

521

TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTCC AAAGAGAATA

200

CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA

243

5 (2) INFORMATION FOR SEQ ID :1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTCCA ATGCACAGTT GCCACATTAA

50

GTCCTGACTG TAGGAAACAC TGATTTGTA AAGTTGCCTT TATTTGCTGT

100

20

TAACTGTTAA CTATGACAGA TATATTAAG CCTTATAAAC CAATCTAAA

150

CATAATAAAT CACACATTCA GTTTAAAAAA AAAAAA

185

25 (2) INFORMATION FOR SEQ ID :1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC

50

TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGGAGCAG GAAATTATG

100

40

AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG

150

522

	TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG	200
	TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCT TCTCCTCAGC	250
5	CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT	300
	CTGTTCACAG TT	312

(2) INFORMATION FOR SEQ ID :1029:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20 ATTATTTATA AATTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT 50
TTGAATTCAA ATTCAATTCAA AAGTTGCACA AATTTATTTC TTTTTTCCTG 100
25 AACATTCCCT TACTTCAGAT TGACAATTCA TTCTATTAG AGCGCTATTT 150
TAAGAAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT 200
TATACAGATG GAAAAAGA 218

30 (2) INFORMATION FOR SEQ ID :1030:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

523

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGTTTAAAC ATTGAATAAA 50
ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT 100
5 TTCTTAGTTC TTTGGACACA TCCG 124

(2) INFORMATION FOR SEQ ID :1031:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

20 TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTCAGTC TGTAGCTTGC 50
CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTTAAGTTG 100
AATGGAATTC AGTTGTTTT TAAAGCTTGT GCTTTTGTG TTCAACTAAG 150
25 GGATATTAGC TTACCATTTT TCTCGGTTGA ATATTATGTG TTTATAGACA 200
AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC 237

(2) INFORMATION FOR SEQ ID :1032:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

ACAGCAACCG GCACTCACTT GGAATCCAG TGTTCCGAGT TCTAAGGCCA 50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA 100
GCGACTTCCT TGAAAGACTGT TTTAACATA CCAAAGGAGG ACAAGCT 147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA 50
GAGGGGGGCA CTAGAACCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC 100
20 TTTTTACTCA TAATTCGCTT CAAGCCAACCT AC GGAGGCGC ATTTACAAAA 150
CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA 200
25 TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTAA 238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

40 TCCATGNCTC NTGGTCTCTG TGCNCTGNC AGGGGCATGC CAGGGCCCTT 50
GGACTGTGCA GGG 63

525

(2) INFORMATION FOR SEQ ID :1035:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCCGC	TCAATGGCGA	AATTCCGAGC	CAGAGCTATT	GGTTGAATGA	50	
15	GTAGCGCTGA	TGGTTTAGAT	AATAACTAGT	ATGGGGATAA	GGGTGAGCAG	100
	GCGCGCCTTG	AGGCAAGAAG	CGGGTTAGAG	CATCTCTACT	TTAAAAGCCA	150
	AAGCCTATAA	CGGTAGCGTC	TACATCACGA			180

20

(2) INFORMATION FOR SEQ ID :1036:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA	TGACATCAAG	GAGTCGATCC	GTCAGCGTGA	CTTGAATACA	50	
35	CCACCGCCGA	CGACCCGAAA	GCCTGATGAG	GAGAAGTCCA	GAATCAGGAA	100
	CAACGGCGAC	ACTCGACTAA	CCATTTAAA	CCAATTGGAA	CC	142

40

(2) INFORMATION FOR SEQ ID :1037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs

526

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

10 CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC 50
TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG 95

(2) INFORMATION FOR SEQ ID :1038:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

25 ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT 50
TTGACAAAAA CATAACACACA TAGTACAGGT AGAACATATA ACTGGTTGAT 100
GCTAAATAAC AGATCCAGAT AATTTCAAT TTGAATTAGC AGCAGGGAGT 150
30 CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT 195

(2) INFORMATION FOR SEQ ID :1039:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

	GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAAGACAT	50
5	TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTC TAAGATGAGG	100
	TTAAGTTCT TAACAAAAGA ATAAACAACT GTGACTCTAT CTGTCGGGG	150
	AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA	200
10	CGAGACTTTG ATGGAGAC	218

(2) INFORMATION FOR SEQ ID :1040:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 318 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		

(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25	TTTATTATTT TGAATGATT TATGGTTTC TACACAATTT ACATCACAAAC	50
	ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATT	100
	CTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG	150
30	CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG	200
	CAAATGCCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA	250
35	CAAGTCCTAC AATTTAAAA AGGCTCGATG GAAAAATTTC TCAATCCTGA	300
	AATCCCCTAG GGAAGGGG	318

(2) INFORMATION FOR SEQ ID :1041:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	

528

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

10	ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
	TGCCGCCGAG GCGGTGGACC GCATCACCGT GGCGCTGACG AACGCGAGAT	100
	TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
15	TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCCGCCG GTGCCGGGC	199

(2) INFORMATION FOR SEQ ID :1042:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 300 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

30	GCCTCTAACAA AAACCTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
	CTTTATACCA AGAACGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
	CCCAGGCAGA CTTCGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG	150
35	ATTGTCCAAA ACAAAAGAAC ATGTCAGCAG GGCCTATGGT GGTTCCATGT	200
	GTGCTAAATG TGTCGTGAC AGGATCAAGC GTGCTTCCCT TATCGAGGAG	250
	CAGAAAATTC GTTGTGAAAG TGTTGAAGGC ACAAGGCACA ATGTCTGGAA	300

40

(2) INFORMATION FOR SEQ ID :1043:

529

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10 GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAAGAGA 50
GTCTGGGATG AAGCGGCCTC CTCCCTGTCT TGCCCTCCAA AATTGAGTCT 100
15 GGCCTGATTC CTTTGAGGAG CAAATTTAC AATCATCCCT CACCCCTAAC 150
CACGGTGAAA CTGGAAAACC 170

(2) INFORMATION FOR SEQ ID :1044:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30 GGCCCCCCCCCT GGGGACTGCT GGTTTCCAGG GGCCACCCCC CCTCATCCAA 50
AAGAAGAACATC AAGTTTTGTT TTCCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100
35 CACCTCGAGC TTCCACTTGG GCCCTTCCC ATGCTTCTAC TTGAGCCCCG 150
CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200
GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCAT 250
40 TTTTTTTTTT 260

530

(2) INFORMATION FOR SEQ ID :1045:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA	TTTAAGGGC	TTAACCTGTG	ACTTTAATAA	GCTGGAACAG	50	
15	TCCACTGAAT	GGGTATAATG	AATTGCAGTA	TATACGTATG	ATCGCTTTT	100
	AAGTGATTAT	CTTTCTTTC	GTAAAGTCAT	GTAAATTTCAT	AAATTTTTG	150
	20	GCAC TGATGT	GTTG			164

20

(2) INFORMATION FOR SEQ ID :1046:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

30	CCCTCCTT	CCGAACCTGGA	GCCCCATCCT	CTCCAGAGTA	TCCAGGGCTT	50
35	CTTCACTCCC	GGGTACCTGC	CCTTCGGCCC	CTTTTCACCA	CAGCTGTGCT	100
		ACTGTCAACC	AGTCTTGCT	GCATAGGCAT		130

40

(2) INFORMATION FOR SEQ ID :1047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs

531

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

	GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC	50
10	AGTGGAAAGCA AAATTCTCAC AATGAATAGC AGTCTTCCA GCTTCTTGA	100
	CACGGATTTC CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG	150
15	TGAATCTCCA TTCGAGGAAG GGGAAAGAAGA GCTCGGAGGG TGACAGCCTC	200
	CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCCTT CTTCCCTCTG	250
20	ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA	285

(2) INFORMATION FOR SEQ ID :1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

	TAAAACGTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA	50
35	CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC	100
	CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC	150
	GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC	200
40	CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA	233

532

(2) INFORMATION FOR SEQ ID :1049:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

	ACTTTAATTT ATTCGGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC	50
15	TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG	100
	AACTCTGAGC TGTCCCTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC	150
	TTAATTCCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT	200
20	CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTC	250
	GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTGGTTCGA TAC	293

25

(2) INFORMATION FOR SEQ ID :1050:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

	AAAACATATAAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA	50
	GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGGCA GATAAAATACC	100
40	AGATCAAAAG TCCTGTTCA GTAATTGAT TAAACTGTAG AATACTAAAA	150

533

AATAAGTTAT TTCTACAGAA ATCTTGAGG GGAGCAAAAA ATCAAATCAC	200
AGTATATACC TAATGGCTA	219

5 (2) INFORMATION FOR SEQ ID :1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTGAT TTTTCGTTT	50
TGCGATAGTT TACTGAGAAC	70

20 (2) INFORMATION FOR SEQ ID :1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC	50
35 CTGCCGATGA TTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC	100
CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTAA	150
TCTCAAAATA ACCACGTCCT TGATACCATT CCCTGTATAAC CAAGGAAGGG	200
40 TATT	204

534

(2) INFORMATION FOR SEQ ID :1053:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

	ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT	50
15	AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG	100
	AGGTATAAAA GGTATCCAAG AAAAGTAAAAA CATAACAAAGG CAATTCAAAT	150
20	CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC	200
	CATAACCGAC AGAAAGTACC GGAATACCCAC CGACACTGAT GTCTTCCAAA	250
	CG	252

25 (2) INFORMATION FOR SEQ ID :1054:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

	AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA	50
	CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT	100
40	TTAGAGGTGT TTAGTATTTC ACTCCGTTCT GATGGAAGCA CTTTGAATGC	150

535

TTGCATGGAG ACATAAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200

TGTATTTATA AA 212

5 (2) INFORMATION FOR SEQ ID :1055:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double.
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAACTGTG CTAACTAAAG TTTTTATTTC ATCAATATAA AAGCTGTAAA 50

20 AAAACTGAGG AGAAAGCACT TGCCAAAAAG ATGAAAGAAA AACAAACATAG 100

AAAACCTTTA AACAGGCCTA AAGTCAGTTC ATAATAAAAGT AACTCATCTC 150

AC 152

25 (2) INFORMATION FOR SEQ ID :1056:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGT 50

40 GAAACCTGAC AACTGACTGT TAGCCTTGTGTC ATCATCCTCA TTGGAGATGG 100

AGATGTTGTA GTCGGAGCCT CATTCTTCC GGGGCAGTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG 200
GCAAA 205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTCTG GGCTCTGGT TACTCCGTCA GAGACTTTGC 50
20 CCTTTGTCTG TTTAAATACA CTGGGAGCCA GAGCTGATTG CCCACCTGCT 100
GCTGTGGTTT TCCGCTTAAC ACAGGGAGAGA TGAGTTGGTC TGGTATATTT 150
GATAGCAGGT TTTAAAATGA ATCC 174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAAA 50
40 GCTTTAAAAT ACCATGTTGA CAGCATTG AATTGTTCA TAGACGTACT 100
TATTTAACTG ATGCCAACAT TCACA 125

537

(2) INFORMATION FOR SEQ ID :1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

	TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTCA AATACTGTCT	50
15	TAGTATATTA AACTCTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC	100
	GTTGAAAACT TAGGTTGTT CCTTCTAAAA TTTCTAAGTC CTTCATTATG	150
20	ACTATAAAGA AAAAAGGTTC ATCAATTCAA AAAAAAATCC TGATTCTCA	200
	AAATA	205

(2) INFORMATION FOR SEQ ID :1060:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

35	ATCTCACAGA TTCTTTTCA CAGATTCAATT CATGTTGAGT GAAAGAAGCC	50
	AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTG	100
	AAAACTAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG	150
40	GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT	200

538

ACTTGGATTT TGGGTCTA 3CTGGCAGG GGAAGGGATA CATTGCAAA

249

(2) INFORMATION FOR SEQ ID :1061:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA 50
AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCAATAT 100
GCAGAACATCAG TGGTTGAAAA AGGAGAAAGA GAGATTTCT TTACAAAAGC 150
20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC 200

(2) INFORMATION FOR SEQ ID :1062:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GAGAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG 50
GATGCCCATC TAAAAGTTAA GTGTCATTTG TTTTTAGATG TTTTACCTTT 100
ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG 150
40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTCCT 200

539

(2) INFORMATION FOR SEQ ID :1063:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

	TATCAAATCA	TGAGTTGAAA	GATTTGACT	ATTGAAAACC	AAATTCTAGA	50
15	ACTTACTATC	AGTATTCTTA	TTTCAAAGG	AAATAATTTC	CTAAATATT	100
	GATTTTCAGA	ATCAGTTTT	TAATAGTAAA	GTAAACATAC	CATATAGATT	150
	TTTTTTACT	TTTATATTCT	ACTCTGAAGT	TATTTATGC	TTTTCTTATC	200
20	AAATTCAAAT	CTCAAAATCA	CAGCTCTGAA	TCTTAGAGTA	TCATAA	246

(2) INFORMATION FOR SEQ ID :1064:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

35	CCCTCATGTG	CCAGTTCGGT	CTGCCTGCAG	AGGCTGTGGA	GGCCGCCAAC	50
	AAGGGCGAGT	GGGAAGCGTT	TGCAAAGCCA	TGCAGAACAA	CGCGCAAGTT	100
	TGAGCCAGAAA	GAGGGCGACA	CGAAGGACAA	GAAGGACGAA	GAGGAGGACA	150
40	TGGAGCCTGG	ACTGAGCCAC				170

540

(2) INFORMATION FOR SEQ ID :1065:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA	CAGGTTCTCA	GCAGTTACTA	AGATGTCCCC	TGATTTCATT	50	
15	GACCTCTGTG	TGTCTTCAGT	CCTTGACCCCT	TTAAGGCTCC	CTGGTGCCAG	100
	AATGTCTGCA	GCTGTAGGAT	CAAAGACCCCT	TGGGGGAAAAA	ATCCATTCTC	150
	AAAAGAGAGG	AAGATGGGGT	G			171

20

(2) INFORMATION FOR SEQ ID :1066:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT	CCCTTACTCA	GTGCAGTTCT	CAAAGTCCTT	TGTATGTCGT	50	
35	ACAGGATCAC	ATCTGTACAT	ATCACACTCT	TGTGGGTAA	GCCCAGAAC	100
	TCATACACAG	CTTCATGGGT	TTACTTTCCC	AAGCACTTCC	TCCCTCCCTG	150
	CAATATCTCC	CCAGCACTTT	CTGCTTCCTA	TCAGCTTTCC	CCTTTTCAA	200
40	C					201

541

(2) INFORMATION FOR SEQ ID :1067:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT 50

15 GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG 100

GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG 150

C 151

20

(2) INFORMATION FOR SEQ ID :1068:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTG 50

35 ATCTGTTGC TCCTTGAGT CTCCCTTTA CTTTACAATC AGAAAACCAA 100

TCGCATACTT CACTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC 150

TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTA 200

40 AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTGGAA 250

542

ACTGACTTTA AAGAAAACAT ACA

273

(2) INFORMATION FOR SEQ ID :1069:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15	CAATCTTGCT TATAAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCA	50
	TCCTGGTGCA ATTGTGATT TTTTTAGCC AAAATGAATG GCAAACTCTA	100
	TTTAGAGCAA AGTAAGTATT AGAAAACCCCT AGGAACCTTT AATCAACGTT	150
20	TATTACACTT TTATAAAGGC AAACTACGCG AAAGAGCCC	189

(2) INFORMATION FOR SEQ ID :1070:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35	TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT	50
	TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG	100
	TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC	150
40	ATGAATCACG ACTTCTCATC CCGTTTATC AGAGTGCATA TACGTCTAC	200

543

TTAAGGAAAA GTAAAACAGT CATTACGAA AGAAAGTCAA TCTGTATCCT 250

AAGCATTAA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50

TACCGCCAGA AGCTAGAACG AAGCACTTCC TCCTAACCGA GTTTTGAAA 100

20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA 150

GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCCAGATA GGCCACCGCGC 50

AGCTCCAGCA TCTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100

40 CACTCTGCAG CCATAGGCC CACTCTGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

(2) INFORMATION FOR SEQ ID :1073:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15	AGTGCCCTAC TCTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG	50
	GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG	100
	GTGGACAGGC TAATTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTCA	150
20	AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT	200
	TCTCTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA	250
25	TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA	300
	TCTATATAGC ACATAGTGT TAAAGACTAA TGAATGCAA	339

(2) INFORMATION FOR SEQ ID :1074:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

40

ATTAATTATG CGGTCCCTCCT CCTGGCAGCT GGACACCAAGT TTGAATCTTC

50

545

	CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA	100
	ATCAAGAAC TCGGACCCAA CTTGGTGCCTA AGACGGATCT CCGCCGATTC	150
5	TGACGGCTCT CCAGGTTTG TC	172

(2) INFORMATION FOR SEQ ID :1075:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

	AGAGTAGGAA GAGGGAGGG AACAGGCATC TAAGATAGAC TTTCTCCATC	50
20	TGTTGGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTCAT ACACCTCAGT	100
	CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG	150
25	CCTGCAAATG AGACCACTCT CATTCTCAG TTTCGATTTG ATTCACTCAC	200
	TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG	250
	GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACTGTTG CTACTGATG	299

30

(2) INFORMATION FOR SEQ ID :1076:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

	GCCCTCATCG GCGATACTGG AGGTTCGCTT TCTCAACCCT GTGGGCTTCA	50
	CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC	100
5	ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG	150
	AATGCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG	200
	CGAGGTTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA	250
10	TCATTCGAAG TATTGCTATG AGCAGTGCAG AAA	283

(2) INFORMATION FOR SEQ ID :1077:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 297 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25	ACCAATCAAG TACACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC	50
	AGTTTCAGCC ACAATTAGC CAAGAATAAG ATAAAAACTC GAATAAGAAG	100
	TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA	150
30	GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA	200
	GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTCAGGC TGGAAAACATA	250
35	TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC	297

(2) INFORMATION FOR SEQ ID :1078:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 291 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

	AATCTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC	50
	AGTGATTGAA CCTTTATTAT TTACCAAGCTA ATATAGTAGG CCCATAAAATA	100
10	GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG	150
	TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTCAGA TAATCATAAC	200
15	ACGCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA	250
	GTTTATATCT AAAGCCCATG TTCTTTGCT TAATATTAGA G	291

20 (2) INFORMATION FOR SEQ ID :1079:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 136 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

	AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAAC ATAAGCGGGG	50
	CTCACTCACC CACCACATTA ACACCAACGAA ACGGGTAATC TAACACGGAGA	100
35	AAACACCCCTA ACGTTCATAC ACCCCATACA CCATTA	136

(2) INFORMATION FOR SEQ ID :1080:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 300 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

	CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT	50
	GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA	100
10	GCTGCGGTAT TAAAAAAATC AAGAATGGAA GCGTTCCCTCA ATTGTCGTTG	150
	AGAATCATAAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT	200
15	CGCGCGTTTC TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA	250
	CACATTGGAG TCACCGGGCC TGC GTAAGAG TATGAAGGTC TTCCTGTAAA	300

(2) INFORMATION FOR SEQ ID :1081:

20

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

30

	GTAAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA	50
	AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT	100
35	ATTGGATGAG ATTTGTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC	150
	TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA	200
	CTGAAGGTGC TGGACATGA	219

40

(2) INFORMATION FOR SEQ ID :1082:

549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10	ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG	50
	AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG	100
15	CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGCCCT	150
	GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC	200
	CATCTGCTGC TATCTTGCC AGTCAGCCAT CACAGTTGG CATCATCAGA	250
20	GTCTCAGCTA GAGGGAGCGT GTCATTTCTG CCTTAGTGGT TTGCCTGCAG	300
	CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACCT	350
25	GTGCGGAAGTT	360

(2) INFORMATION FOR SEQ ID :1083:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

40	CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT	50
	CTTTCAATTAA AATACACTCC AAGACATCGA GTTGGCAGA TATTGCGCCC	100

550

	GCCGTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT	150
	AGACATTTGC TTGAAATTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT	200
5	GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAAA AAAGTTCCAG	250

(2) INFORMATION FOR SEQ ID :1084:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

	TNCTAGATAAC NTCCCTCTGT CTCACATTCA TAGTGTGTTTC TTGTCTAGTG	50
20	TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTG GGGAGAGTGA	100
	AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG	150
25	GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTTAAA	200
	AAATTAAAAA GAGGATTTT AAAAGGAATA TCTTGTCAA AATTTNTTAA	250
	GTTTTAATAG G	261

30

(2) INFORMATION FOR SEQ ID :1085:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

	GCAATCCATA AGTGTCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT	50
	CTTCATGATC TTTTCGATT TTAAAATGTC ATGCAATTTC AGAGAAAAGC	100
5	TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA	150
	TCACTTTTC ACTTTCCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC	200
	TTAATACACC AGACAAGAAC ACACTATGAA TGCGAGACAG AGGGAGACAG	250
10	AGGC GAAATA	260

(2) INFORMATION FOR SEQ ID :1086:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 213 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25	AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAAGA CCTGGATTTT	50
	TCGGAAGCTA TGGATTGAG GGAAGACAAG GATTTCTGG AAGACATGGA	100
	TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA	150
30	CGAATTCCT GGAAGACCCG GATTTTCGG AAGCTATAGA TTTAAGGGAA	200
	GACAAGACGG ACT	213

35 (2) INFORMATION FOR SEQ ID :1087:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1087:

5 TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG 50
5 TTTAGGCATT TGGAAAATCT GGTCACATC ATAAAGAACT TGATTGAAA 100
5 TGTTTCTAT AGAAACAAAGT GCTAAGTGT A CATATTATA CTCGACGTCG 150
10 ATCATTCTC AGTCCTATTT CTCAGTTCTA TTATTTGAGA ACCTAGTCAG 200
10 TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT 250
10 TTTTTT 256
15

(2) INFORMATION FOR SEQ ID :1088:

20 (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 264 base pairs
20 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear
25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

30 TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC 50
30 TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG 100
30 GCTCTGACAG TGACAGGTTTC TTCCCTCTGA AAAAAGAATA GAAGAGGAGC 150
35 TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA 200
35 AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA 250
35 CTGAGGGCAG AGGC 264

(2) INFORMATION FOR SEQ ID :1089:

(i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTCGT CTGTTCAGTA GACTCCGATT TCAGAATATG	50
	TCGGAATTTC AGACTCCGGA ACTTTGAGA ATGTCATTAC AGGAACCTTG	100
	TTTACATACC GAGCTGTTAG CCCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

(2) INFORMATION FOR SEQ ID :1090:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 366 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA	50
	CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAAGT CGATGAGAGA	150
35	GAAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTGGT	200
	CAAGTAATGG AAACCTTTGA CTACTAGTGT AAGTCAAAAG ACAAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTC TCTATTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAA	350

554

AAAAAAACATA GATGTT

366

(2) INFORMATION FOR SEQ ID :1091:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15	GGTCTGAATC ATGAAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC	50
	AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTCA	100
	CACCATATGA AGACATCAAA AAACACTTAA GGATTCGAGA AAGAGAACAT	150
20	CTTTTGTAA AGAAGAGAAT AAGATTTGG AAGAAAAAGT AATAGCAAAT	200
	TTGAAGAAGA AACAAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA	250
25	TCATGCATAT CGAGAGGTAA ACATTGATAG AGATAATTTG AAGAGCAAAT	300
	GGACA	305

(2) INFORMATION FOR SEQ ID :1092:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

AAATGGAAGT TGAAC TGAGT GTGGTTCCA GTACAGGGCA TCTGGCCACC

50

555

	TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT	100
	GCCAGAGACA GCCAACACA GGAGACATGA CAAATTACTA TCATCTTTG	150
5	CTTCTTTATT TTTATTATTA TTATTTTCT TTTGTGGAG AACAGCGTCT	200
	TGCTGTATTG CCCAGCCTGA TCTCAAACTC CTGGGCG	237

(2) INFORMATION FOR SEQ ID :1093:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 420 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20	AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGGAAGTGCA ATATCAAGGT	50
	GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA	100
25	GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA	150
	CAGTCTTCCTC CATGTGTATC CTTCCCTCAG TTTCCCTTAT AGGACACCAAG	200
	TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTGAGT TACTCAG	250
30	CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTAA GGAACTAGGA	300
	CTTAGGGCTT ACAAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTAA	350
35	AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATAACACACA TTAAGGTTG	400
	TGGGATTCAAGAAAGGTATAC	420

(2) INFORMATION FOR SEQ ID :1094:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 192 base pairs

556

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

10	GTTCCTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
15	CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTC TCCATAGGAG	100
20	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
25	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192

(2) INFORMATION FOR SEQ ID :1095:

20	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 228 base pairs
30	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

30	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
35	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC	100
40	ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTT CACCAGCATT	150
45	GCCAAACCAAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTTCT	200
50	GCTTCTTGGA TACCTCCTTC AGGAAATC	228

(2) INFORMATION FOR SEQ ID :1096:

40	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGTH: 198 base pairs

557

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

10	ATTTTTATG GAAAAAGGG GATAATGCAA AATAGCAAAA ATTGTAAACA	50
	AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTAAAACACC	100
	TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTTCATTAC	150
15	ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT	198

(2) INFORMATION FOR SEQ ID :1097:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 118 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

30	TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG	50
	CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTTCTAC AAAACTGTGA	100
	CACTTCAGTC AGTTTTTC	118

35 (2) INFORMATION FOR SEQ ID :1098:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 138 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

558

(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5 AAAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACCA CTCCAGCAGT 50
5 CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNNGGACTCG 100
TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCGNAAGG 138

10 (2) INFORMATION FOR SEQ ID :1099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

ACTCCACCCAC TGGGNCCGCC ATGTTTGGG TNNGNGCAAT GCGCTGTCTG 50
TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT ACAGTGACTG 100
25 ACAGTGCCGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG 150
G 151

30 (2) INFORMATION FOR SEQ ID :1100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT 50

559

	CGTGTAAGTA CACTCTATAT TGGCACAAACA TAAAATTAAC TAGTGACGCA	100
	TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT	150
5	CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG	200
	C	201

(2) INFORMATION FOR SEQ ID :1101:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

20

	TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT	50
	CGTGTAAGTA CACTCTATAT TAGCACAAACG ATAAAATTAA CTAGTGATGC	100
25	ATTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG	150
	TATCACTGGA GGACTGGNC CAGGACCTGA CCTGGTGGTA CCAAAATCCA	200
	TGAGGCNGNA AT	212

30

(2) INFORMATION FOR SEQ ID :1102:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG 50
GTTCGTGTAA GCACACTCTA TACNNGACA ACATAAAATN AACTAGTGAT 100
5 GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC 150
AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN 200
GAGTGGAAAT TCCANCAT 218

10

(2) INFORMATION FOR SEQ ID :1103:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT 50
25 TCGTGTAAAGT ACACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG 100
CATTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA 150
GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC 200
30 ATGAGCG 207

30

(2) INFORMATION FOR SEQ ID :1104:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

561

(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

	GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG	50
5	ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC	100
	TCTGCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCCCTGAAC	150
10	AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT	200
	CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN	250
	GTGNAGGCC	259

15 (2) INFORMATION FOR SEQ ID :1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

	ACATGACCCC TTGGACTGAA GGCGCTCACT AGTAAAGGAG TGTCAATGCAG	50
	GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA	100
30	CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG	150
	CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC	200
35	ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT	230

(2) INFORMATION FOR SEQ ID :1106:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

	ACATGNCCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT	50
	CAACACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA	100
10	GGACTTTGGG GGGGAGTGGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG	150
	GTNAGAGGGG GCT	163

15 (2) INFORMATION FOR SEQ ID :1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

	ACNTGATGAT TGCCATTATT CTGTGCTAGT GGCTAGAGGT AGACCCAATA	50
	GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT	100
30	GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA	150
	GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT	182

35 (2) INFORMATION FOR SEQ ID :1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

	CCCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTATGC AGGTCAACAC	50
5	ATGTCGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT	100
	TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG	150
10	AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT	200
	CGNGCCTTGA AAGA	214

(2) INFORMATION FOR SEQ ID :1109:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 133 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25	ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTATGCAG	50
	GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC	100
30	ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT	133

(2) INFORMATION FOR SEQ ID :1110:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 156 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

	GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTCA	50
	CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA	100
5	TGCACGGGGG ACTTCTGGGA CGAGAGTGCA TAGGATACTT GTCTGTGACT	150
	GGAATG	156

(2) INFORMATION FOR SEQ ID :1111:

10	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 282 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
15	(D) TOPOLOGY: linear

20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1111:	
	GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCGC	50
	AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC	100
25	ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA	150
	AGACACATAC ACTAACACGT TCATGGAGCA CTATTACAC AGCAAAGACT	200
	CGATCAACTC ACACACTCAT GAATGCCGAT CGAAATAGAA GATGTGGTAT	250
30	GCATACACCA CGAAATACTA CGAGCCATAA AA	282

(2) INFORMATION FOR SEQ ID :1112:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

565

(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

	TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA	50
5	ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT	100
	CAAAAGGAAA TAAANNGNCN TGTNAAGAC CATAACACNAT NGTCCATCGG	150
	AGCCCGTATN CACGCAGCTT GTCATAACTA T	181

10

(2) INFORMATION FOR SEQ ID :1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- 15 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

	ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG	50
25	AACTTAAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA	100
	TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT	150
	AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA	200
30	CACTCATGAA TGCGGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA	250
	AATACTACGA GCCATAAAAG GCGAAATC	278

35

(2) INFORMATION FOR SEQ ID :1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- 40 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTG 50
5 TGAGCCATAC AGTTTTGTT GCAACTAGTC AACTCTAAC TNACGTGGAC 100
AGCATGTAAA GAACGAGAGT GACTG 125

10 (2) INFORMATION FOR SEQ ID :1115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCCGGGA CCTGCAAAC TTTTGAAAG 50
ACCAGATAGT AAGTATTTA TGCTTTGTA GCCATACAGT TTTTGTGCAA 100
25 CTAGTCAAAC CTCAACTCAC CGTGGACAGC ATGTAATGG ATGGGAGTGG 150
CTGCCGG 157

30 (2) INFORMATION FOR SEQ ID :1116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTA AGACCAGATA GTAAGTATT TATGCTTG 50

567

GAGCCATAC A GTTTTGTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100

GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTGTA AAGACCAGAT AGTAAGTATT TTATGCTTG 50

TGAGCCATAC AGTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC 100

20 AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTT 50

GTGAGCCATA CAGTTTCGT TGCAACTAGT CAACTCTCAA CTTCACCGTG 100

GACAGCATGT AAATGGATGG GAGTG 125

40

(2) INFORMATION FOR SEQ ID :1119:

568

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10 (xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT 50
CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT 100
CAAAGAGCCA ATGAGAAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA 148

15

(2) INFORMATION FOR SEQ ID :1120:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT 50
AATCAAGAAA AAATAGCACC AACAAACAATG AGGAGAAAAT GGAAAAAGGG 100
CAGAGTATTG CAAAGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT 150
35 TAAGCCTTCA GTTGCCCTG TAAGCAAACG GAAGACGTGC AAGTCATCCT 200
TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAAATTAG 240

30

(2) INFORMATION FOR SEQ ID :1121:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs

569

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

	AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG	50
10	GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA	100
	AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG	150
15	ATTTTTAAGC CTTCACGTCT GCCCTGTAAG CAAACTGAAG ACGTGCAAGT	200
	CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGCA ATGAGAAGGG	250
20	ACAG	254

(2) INFORMATION FOR SEQ ID :1122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

	AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC	50
35	NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA	100
	TGGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA	150
	ACGAATGATT CTTAACCTT CACGTTGCC CTGTAAGCAA ACTGAAGACG	200
40	TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAAC	250

570

GAG

253

(2) INFORMATION FOR SEQ ID :1123:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15	AAATGGGAG AATCACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT	50
	GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAAATCCGA GAAAATGGAA	100
	AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT	150
20	GATTTTTAAG CCTTCACGTC TGCCCTGTAA GCAAACTGAA GACGTGCAAG	200
	TCATCCTTTG	210

25 (2) INFORMATION FOR SEQ ID :1124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

	AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC	50
	CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA	100
40	TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC	150

571

AACGAATGAT TCTTAAGCCT TCATGTTGC CCTGTAAGCA AACTGAAGAC 200
GTGCAAGTCA TCCTTGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAAG ATGTCACTCA AGAATGCGCC 50
20 CGTGGCCCTC CAGTTCCCTGC GCACTAAGAG CGTCCCGCT 89

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50
35 ACCAAAACCTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100
ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150
40 ATGCTACTGG ACACATGCC ACACAATAAT ANTCAANRTGT NTYGTTAGGC 200
CTACT 205

572

(2) INFORMATION FOR SEQ ID :1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG GCCGACAACA CCCTTATTGC TAAAGTAAAT AATGNCGCGC 50

15 GGGGCCTGGA CCACCCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG 100

TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA 150

20 A 151

(2) INFORMATION FOR SEQ ID :1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCCCTACCC CCCTCAGCAA 50

35 GCCGGAGAGG CTAGCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC 100

CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT 150

GACAGACGAG ACCTGCCAGG ACGCAGCCAT TGCGGGCTGC AAGGCCTCRC 200

40 CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT 237

573

(2) INFORMATION FOR SEQ ID :1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

	GCCTCGTGGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG	50
15	CACCAACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT	100
	CCTTAAGATC ATCCAACATAT AGGATG	126

(2) INFORMATION FOR SEQ ID :1130:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

30

	GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG	50
	AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT	100
35	CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG	150
	TTTATTTGCA AGGATTTTC TTTCGRGGGC GGAGGGGAGA GAAAAGTAAA	200
	TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCCTT YGTATC	246

40

(2) INFORMATION FOR SEQ ID :1131:

574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10

CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATT ACCGAATTAA	50
TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT	100
15 TTTCACCCCTC AAAGTATAAA AAGTATGAAA NATAAACAAAG CTCTTGCACT	150
GTACACTTAG AAGTGTACAA TTAAAGCATT ATAGAGCTAT CTACACACCG	200
20 ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG	250
TGCAGACAGA ACTAAAACCA ACT	273

(2) INFORMATION FOR SEQ ID :1132:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35

GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG	50
TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAACCTAT TCAGTGCTCC	100
40 CTTAGACATT CTTCCAGGCA GGATCAAAC TCAAAGGAAAA GGAATTGTG	150
AAGCAAACCA TGGCTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG	200

575

	AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA	250
	AGCCAATGTA TCTGACCCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT	300
5	ATTTCTGTTT GTTAAAAAGT TCAGAATT	329

(2) INFORMATION FOR SEQ ID :1133:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

	CCCCGAGCTA GTTGTCCCCGA CCTG	24
20		

(2) INFORMATION FOR SEQ ID :1134:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

	GAGGATCCAC AAACCATGGA ACACCTCTCGC GGCTGCCACT CCCCCATGAC	50
35	CACCCCTACAG GCCCTAACCC CAGCCCCCTCA CGTTATCGTC CAGCCACAAA	100
	TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG	150
	CGGCCCCCTGC CGGGCACCCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT	200
40	CCAGGAATCT CTACCCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA	250

576

CCAAACCTCG CCAGAAGGCT TCTTTCGGG TTGATGCCA TCTATTY

297

(2) INFORMATION FOR SEQ ID :1135:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15

GCCGCTTAC TGCTCAGTTC GGAGCTACCG CTTGAAAGC AACAAAAAAG

50

CNTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA

93

(2) INFORMATION FOR SEQ ID :1136:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30

CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG

50

TTGTGGGAGA TAACGGTGGC ATAGTTCCCT GATGCCCGGG CCAGCTTGCC

100

35

ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA

150

TGGTGCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTGCCG

200

40

CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC

250

CGCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG

300

577

GCCCTCRAA CCCGGGCTA TACACGTCAA AATC

334

(2) INFORMATION FOR SEQ ID :1137:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15	CGAGGATCCG CATAACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG	50
	ATGAAGAAC TCCAAACCCCT TTGACAGCTC CTCGGGTNA AACCTGGNAY	100
	AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT	150
20	CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT	199

(2) INFORMATION FOR SEQ ID :1138:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35	CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCGCGT	50
	GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG	100
	TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC	150
40	ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG	200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT 250
TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG 300
5 AAGG 304

(2) INFORMATION FOR SEQ ID :1139:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

20 GAGGATCCGG GTACCATGAG AAACTTGAA GCCAGAGATT TTAAACAATC 50
AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA 100
CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC 150
25 CTTTAATAGT TATCTAAATG CAGAGTTGT TTATGAAATG AACCAAAGCA 200
GTTTGTCAATT TCTTACTATA AAATACCGAA AATAAAAGTGC AAAACTTAGC 250
CACTACTGGC TAAAGAAAATC AAGTAAA 277
30

(2) INFORMATION FOR SEQ ID :1140:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

579

	CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCAA	50
	AAGAGAGCTC CCTGAGAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT	100
5	TTTAGCAGAG CAAATTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG	150
	GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTTCA GACTGGGCTC	200
	CAGCTTCT	208

10

(2) INFORMATION FOR SEQ ID :1141:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 274 base pairs
15	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

	CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG	50
25	CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG	100
	TCAACAAATGG TTAACTTCAG CCGTACATTG CTTTCCTGAA GCTCATAACT	150
	TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACHTT	200
30	TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT	250
	GTCTCACCAA TACAAAGGAT GTTG	274

35

(2) INFORMATION FOR SEQ ID :1142:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 226 base pairs
40	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

580

(xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

5 GCCTGCACAT TGACTGTGGG AAACTCGGAA ACAAGCTCAC ATCTCCCCGT 50
5 GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAACTG CAGTTGCCAC 100
10 CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA 150
10 TTTCTCCTAA AAGATGGCAG AAGATTTAA AGTCCCGGCT GATGGAGTTG 200
15 TTAGTGTCCCT ATGGTAACAC CTTCTT 226

(2) INFORMATION FOR SEQ ID :1143:

15 (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 168 base pairs
20 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25 RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRG 50
30 TGRCRCGNTG NCNGTGAGGR CRTGNRGNC CRTGCGAGTG GGCTTACCGN 100
30 TAGGTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG 150
35 GNANGRTGNN GTGGAGRG 168

(2) INFORMATION FOR SEQ ID :1144:

35 (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 256 base pairs
40 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

581

(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

	CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT	50
5	TCTTGAGGGA CCTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTGC	100
	CAGGATTTGA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT	150
	CCACATAAGG GCTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT	200
10	AAACAAACCTT ATAGTGTGTT CGCTTTGAAT TGTATGAATT CTTAGAACTG	250
	AGAAGT	256

15 (2) INFORMATION FOR SEQ ID :1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

	AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA	50
	GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG.	100
30	TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT	150
	GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG	184

35 (2) INFORMATION FOR SEQ ID :1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

582

(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

	CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG	50
5	CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG	100
	ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT	150
10	TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG	200
	GTGCTGAGAA GAATGCACAA G	221

(2) INFORMATION FOR SEQ ID :1147:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 255 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25	CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT	50
	TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT	100
30	TAAGGATTCT CACATTCAAG ACAGAGAACAA ATTNTTTAA TGAATCCATC	150
	CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC	200
	RRTMATTCTT AACANCAAAC NGMGMCTGNN NTCCCRNCTT ATAACCMAAA	250
35	GATNT	255

(2) INFORMATION FOR SEQ ID :1148:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 230 base pairs
	(B) TYPE: nucleic acid

583

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

	CGAGGATCCA GGTACCATGG ACGATTACCA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTCACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC	150
	CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
15	AGTCGGTGAC GCCCGATTTG GATCGGGTGT	230

(2) INFORMATION FOR SEQ ID :1149:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 223 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30	GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGGAGGA GGTTGAGACG TTCTCCTTTC	100
	AGGCAGAAAT CGCCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
35	AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAAATT CGATATAAAA GCT	223

40 (2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGA ...TC CTAATGCCCT	100
	ATGATCACGT GGAACTAACA TCAATGACA TGAAGAACGT GCCAGAAGCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAAAGG ATGCGATGGG TATTTCGTGA NGCTATTGAA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

(2) INFORMATION FOR SEQ ID :1151:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 140 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

35	TGAGGATTAA TAGATTANAG CTAGAGTTCA CATTATGG ATTACAACCA	50
	AAAAAAACCT GAAAAAGAAA AAAAACAAAAA AAGCTAAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTT AAACCCCCAA AGCAACCCCC	140

40 (2) INFORMATION FOR SEQ ID :1152:

(i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCCGGT ATCAGCAGAG GCGTGTACGG	50
	GCAC TGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG	100
	GTCACCAAGG TAGATTCCA GCAGCCTAGT CCAGCTGAAC GCTTCCAGC	150
15	CTTGCTTTTG AGCAGCTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

20 (2) INFORMATION FOR SEQ ID :1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1153:

	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAAT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACCCAG	150
	GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCAGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA	250
	GAMGCCNNMAC AGGGCTRGGG ACTG	274

586

(2) INFORMATION FOR SEQ ID :1154:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

	GAGGATCCAC CGACCATGGA ACACCTCTAA TGGCTGCAAC CACCCCGTGG	50
15	CCCCCTTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA	100
	CCAACAGCTG CAGCCCCCTGA GATCTTCACC TTAGACCCTC TCCCCGAAGCC	150
	CGCAGCCGCC CCTGCGAACCC CTCCAACCTCG TTACACCGCG CCGAAAGCCT	200
20	ATTCCCAGGA CTCTCTGCCCTACGTGACC GNCCCTAGCT GCTAGTCGAG	250
	AATCCGAACT CCGCTCC	267

25

(2) INFORMATION FOR SEQ ID :1155:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

	CTCAAACCCC GNTTCCCCCC TAATAAGAGC AACTAAAAAA CTTCTGATAA	50
	CCACAATAAA AGCGTGCATT TGAGGCACAAT TCAAAAGCCA ACCCCCTTCGA	100
40	AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG	150

587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200

CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCA TCCACACCTG 50

20 CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG 100

GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCCCGGCTCT 50

GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCACA AGGGCAGAAA 100

GGTGAGCCTT ATGCACTGCC TAAAGA 126

40

(2) INFORMATION FOR SEQ ID :1158:

588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA

50

CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT

100

15

T

101

(2) INFORMATION FOR SEQ ID :1159:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

30

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG

50

GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC

100

CCACACACAG GTGGCGGTGC GGGTGAAC TG GAAGGGGAGG TCGAAGGTGC

150

35

CATCTTCTTC AGGCCCCCTCC AC

172

(2) INFORMATION FOR SEQ ID :1160:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

589

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

	GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA	50
	TGGTTATTTC CCAGGACCAC ACGATTGCC TACGTCACTG GAAGGCTATG	100
10	TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG	150
	CTTTGACCCCT GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT	200
15	TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT	235

(2) INFORMATION FOR SEQ ID :1161:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 284 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

	GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG	50
30	TTAGATACAA ATGCAAAACG CTTCTAAAA AACGGCCTGA AAAAAAAACTC	100
	ACAGACAATG CCAAACTTA TAGGTCTGTA TTTCTCTTTA TACAAAATGC	150
35	CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG	200
	ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA	250
	ACCCTCATAA AGCCTAAAA GTACATTGT GAAA	284

40

(2) INFORMATION FOR SEQ ID :1162:

590

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10	GCTCACATAA ATTTCTTCAC CGACCCTTT CCTTCCAGCT TCCTTACTAT	50
	AAAAAAACCCC ACA AATA TGTTCATCAT CATCCATACT AACCAACCCC	100
15	GTCACCACATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG	150
	TTACCACCTC TAGGGGCAGA CCCCTTTCA GATATATTCA AGAGTTAAT	200
	ATCCTCCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA	250
20	ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC	287

(2) INFORMATION FOR SEQ ID :1163:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 122 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

35	GAGGATCCAA AAACCATAAA ATTCACTCATC CCCAGCAGGT GCNCTAGCTA	50
	TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANN TCGTATAGAT	100
	AAACACCAAT CATGGGTCGG CC	122
40	(2) INFORMATION FOR SEQ ID :1164:	

591

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10 GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG 50
GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC 100
15 CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT 142

(2) INFORMATION FOR SEQ ID :1165:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

30 TATTCCCCCG GTATCAGCAG AGGCGTGTAC GGGCACTGCT TTAAAACCTGG 50
GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC 100
CAGCAGCCCT AGTCCAGCTG AACACTTCC AGCCTTGCTT TTCAGCAGCT 150
35 TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG 200
GATGAGAATA GAGAACTCA 219

(2) INFORMATION FOR SEQ ID :1166:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs

592

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

10	GAGGATCCAC CAACCATAAGA AAGGAAACAA CACTTGGAGT GAACCCGACC	50
15	CAAGCCACTA CACCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA	100
20	AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTNT CAATCCAAAC	150
25	ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC	200
30	AA	202

(2) INFORMATION FOR SEQ ID :1167:

20	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 159 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:

30	GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAAATG ACCTTTACGA	50
35	AGACACGTCT GATAACCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG	100
40	GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC	150
	ATCTGGAGA	159

(2) INFORMATION FOR SEQ ID :1168:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs

593

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

10	CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG	50
	CGATTGCCAC CGCTTCTCTC TAGTCTCACG AGGGGTTTCC CGCCTCGCAC	100
	CCCCACCTCT GGACTTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC	150
15	CAGCGCTTAG GTCGGAGCGA GCCTGGGCC ACCGCCGTGA AGACATCGCG	200
	GGGACCGATT C	211

(2) INFORMATION FOR SEQ ID :1169:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

30	GGATTTCCGG TCCTGGCTTT CTGATATTC TAAAATCGAC CTGGAATCAA	50
	CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC	100
35	CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT	150
	TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG	200
	ATGAACACTT T	211

40	(2) INFORMATION FOR SEQ ID :1170:
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594

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10

GAGGATCCGC GCAACCATAG AACTCACAAAC CCAGCCATAT ACCTCAGACA	50
CAATGGAATG GGCGGAGGTC GAGGTNGACA AACCCCTGAGT AATGTTGGC	100
ACTTCCGCAC CGGAGCTGTT CTTACCTTG ATAAAGTGGA TGTTATTGCT	150
ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC	200
CTATCCACCA ACGNCGAACCA ATATGCTGTT GCCAMGATTG AGCACCGAGCC	250
20 GTTTGGGCTC AACGGC	266

(2) INFORMATION FOR SEQ ID :1171:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35

GGCACAAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG	50
CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG	100
40 GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTGAGGGC	150
TTTAATCCTT TAAAAC	167

595

(2) INFORMATION FOR SEQ ID :1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

	AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC	50
15	TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG	100
	ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT	150
	TACTGAGGAT ACGCAACTCA TAAAACTCTA CTTAAAGCAA CAGGGCAGAC	200
20	GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC	232

(2) INFORMATION FOR SEQ ID :1173:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

35	GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT	50
	CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC	93

(2) INFORMATION FOR SEQ ID :1174:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs

596

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

	GCCTTTTTT ACCCGCCGGA AGCTACAGCT TTTGCCCCC CAAAAAAACC	50
10	CCACCCCTTT ACCCACCGCG GACCCAAAAA CAGCAAAAC CAAGGACCTC	100
	TCCCAACCCC AACCCCTCCT TTTTGGCCCT TCCTTCCCCC CCTCCCAGCC	150
15	CACCCCCAGA CACCTCAATC CCCCAAAAGG ATGCCCTAAA CCTCTCCTAA	200

(2) INFORMATION FOR SEQ ID :1175:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 121 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

	GAGGATCCAA AAACCATGGC ATTCAATCACG CCCAGCAGGT GTCCCAGCCA	50
30	TGACTTACCA TAGCAAAACA CAACCACACA CTAACCTGCA TCGCCTAGCT	100
	TACTGATGAT GATGTCCTGG T	121

35 (2) INFORMATION FOR SEQ ID :1176:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 26 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTTGCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAAGTTCAAG TCAA

144

598

(2) INFORMATION FOR SEQ ID :1179:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

	GACCAGGGAG GAGGTTAAC	50
15	CAACTTGGAC CCCCTCCGGC CTAGCCGCCG	
	AGGAGGTGCA TTCCGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG	100
	TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCACGCT TTGATTTACT	150
20	GATCTCGCTG AAAAGACAGA CGCTTTAGA TACCGAGTCG ATAGGGGTC	200
	TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT	233

(2) INFORMATION FOR SEQ ID :1180:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

35	CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC	50
	CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA	100
	TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAACGCCGC GAGCCCCCTT	150
40	CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG	200

599

AGGTAGACGG GACCAAGATC TGCTG

225

(2) INFORMATION FOR SEQ ID :1181:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15	TGAGGATTAA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC	50
	GATGAATAAG CTTGATGTGG CCTAGTTTN NGNNNNNTGG NYATGGTNNA	100
	TCNNNTTANT TTTTGGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG	150
20	TTTAGAGTTT GGAAGCGGCN RNGCGTARMG NNACTCYACG CTCGCNNCTN	200
	TTGNNNNACA GMRGGNCTC TNGGRTGAGT GGRTNCMGTG GGMGGNNTCN	250
25	NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTGNNGCTN GCT	293

(2) INFORMATION FOR SEQ ID :1182:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

	GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTTTTCT TTTTCTTGGC	50
40	GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA	100

	600	
	CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA	150
	GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCAATTCC	200
5	TTCTGGCTGT TGAGACCCCCG TGGACTCCCC TGGATTCCAG AGNNTNATT	250
	NG	252

(2) INFORMATION FOR SEQ ID :1183:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

25

ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG

50

AAACTGTAGA TTCCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG

100

25

AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT

150

ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT

200

GT

202

30

(2) INFORMATION FOR SEQ ID :1184:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTCGTGG TTCACAATTT CTTCAAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15

ACCGTCCTTC TGGTTCATCC TAGCAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

30

ACATCATCCG AGTCCCCTCT ACAGTGTCA TTGTGATCGT TGCATCCCC

50

TGGTTTGGAA ATAAAATATA AACTGCCCGG CAAGAGATAA AATTGTATTT

100

TTTA

104

35

(2) INFORMATION FOR SEQ ID :1187:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

602

(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

5 CTGGTTCTGT TTCTCGCAGG TGCTAGAGGG GAGGCTGTCC TCTGGTCAGG 50
AGAACCTAT TCAGTGCTCC CTTAGA 76

(2) INFORMATION FOR SEQ ID :1188:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA 42

(2) INFORMATION FOR SEQ ID :1189:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

35 GGCGGACGTG CGCGCCTTGT CTTCGCGGCA CCTGGGCCTG AGGTGCGTGC 50
CTCCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC 100
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC 150
40 GCCAAGGCCT TTTATTTATG GCTAGTTGC TCTCGTAAA TACTAACATC 200
GTTTTAATGG CACTCATCAA GTACGCAAAT GATATGATT AACCTCGCGC 250

603

AAT

253

(2) INFORMATION FOR SEQ ID :1190:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15	GAGGATCCAC CAACCATAAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG	50
	TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAAA	100
	CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT	150
20	GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC	200
	AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT	250
25	TT	252

(2) INFORMATION FOR SEQ ID :1191:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

40	GAGGATCCAA CAACCATAAGA GCACATAAAA ACCGCCAAC GATCTAACTA	50
	ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC	100

604

TGCCGANACC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA 150

CCCTTCCGGC TGCCCTTGTG TTGACTTG 178

5 (2) INFORMATION FOR SEQ ID :1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCAG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT 50

20 CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT 100

GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNNG 150

NGGGCA 156

25 (2) INFORMATION FOR SEQ ID :1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTGT AATACAGACA 50

40 TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA 99

605

(2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACA GACA

24

15

(2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTCGC AGGAGAAGGA

20

30

(2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

40

AANNTCTCGG ACAGTGCTCC GAGAAC

26

606

(2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNNTCTCGG ACAGTGCTCC GAGAAC

26

15

(2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

(2) INFORMATION FOR SEQ ID NO: 1199

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG

23

607

(2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

(2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCG CAGGAGAAGG AA

22

30

(2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

40

CTGTCTGTCG CAGGAGAAGG AG

22

608

(2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

(2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG

24

30

(2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

GATCCGGCTC GAGT

14

609

(2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG

18

15

(2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO: 1208

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

40

CGAGGGTCGAC GGTATCG

17

610

(2) INFORMATION FOR SEQ ID NO: 1209

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

(2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT

50

TTTTTT

56

30

(2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

GCCWSCGCCG A

11

(2) INFORMATION FOR SEQ ID NO: 1212

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 1213

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

30

TTGACACCAAG ACCAACTGGT AATG

24

35

In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40

85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

5

10

15

CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-
 - 5 (a) a sequence selected from SEQ ID Nos 1 to 1193;
 - (b) an allelic variation of a sequence as defined in (a); or
 - 10 (c) a sequence complementary to (a) or (b).
2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
- 15 3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of 20 the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.
- 25 6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
7. A nucleic acid sequence as claimed in claim 2 or claim 3 and 30 encoding at least a portion of a biologically active polypeptide.
8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.
- 35 9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
- 40 10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a 5 gene.

12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.

10 13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said 15 fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

14. A vector as claimed in claim 13, wherein said vector control or 20 regulatory sequence comprises a regulatable promoter.

15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.

25 16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.

17. An antibody directed against a polypeptide obtainable by the 30 performance of a process as defined in claim 16.

18. An antibody as claimed in claim 17 and which is monoclonal.

35 19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.